

Om protein - protein search, using sw model							Copyright (c) 1993 - 2000 compugen Ltd.
Run on: March 27, 2002, 15:34:44 ; Search time 15.93 Seconds (without alignments) 1898.387 Million cell updates/sec							Gencore version 4.5
Title: Perfect score: Sequence:	US-08-774-104A-2	1 MMVYHETRALAQSDLQOLYA.....ETGILKFEPMRQLKLDYHVE 397	Scoring table: OLIGO	Gapop 60.0 , Gapext 60.0	Searched: 219241 seqs, 76174552 residues	Word size : 8	Total number of hits satisfying chosen parameters: 30
Minimum DB seq length: 0	Maximum DB seq length: 2000000000	Post-processing: Listing first 45 summaries	Database : PIR 68:*	1: pir1:*	2: pir2:*	3: pir3:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
SUMMARIES							
Result NO.	Score	Query Match Length	DB ID	Description	RESULT 1	ALIGNMENTS	anthranilate synth
1	10	2.5	511	T36506	Query Match Best Local Similarity 2.5%; Score 10; DB 2; Length 511; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RESULT 2	anthranilate synthase (EC 4.1.3.27) alpha chain - Haloferax volcanii
2	10	2.5	523	A42301	C;Species: Haloferax volcanii	Query Match Best Local Similarity 2.5%; Score 10; DB 2; Length 511; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	C;Species: Streptomyces coelicolor
3	10	2.5	526	T49199	C;Accession: A42301	C;Accession: T36306	
4	10	2.5	613	T50034	A;Status: preliminary; translated from GB/EMBL/DDBJ	R;Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, I submitted to the EMBL Data Library, March 1999	
5	9	2.3	396	A40365	A;Molecule type: DNA	A;Reference number: 221604	
6	9	2.3	404	D86716	A;Residues: 1-511 <SAU>	A;Cross-references: EMBL:AL035654; PIDN:CAB38585.1; GSPDB:GN00070; SCOBDB:SCE8.07C	
7	9	2.3	411	B64540	A;Experimental source: strain A3(2)	C;Genetics:	
8	9	2.3	433	T43924	A;Gene: trpe2; SCOBDB:SCE8.07C	C;Superfamily: anthranilate synthase component 1	
9	9	2.3	434	A75163			
10	9	2.3	462	S03316			
11	9	2.3	471	A69557			
12	9	2.3	485	S75555			
13	9	2.3	494	E70352			
14	9	2.3	494	JX0065			
15	9	2.3	502	C83857			
16	9	2.3	508	S19366			
17	9	2.3	508	S75537			
18	9	2.3	512	JH0098			
19	9	2.3	515	I_NBSI			
20	9	2.3	621	S27752			
21	9	2.3	621	JQ1685			
22	8	2.0	141	E83345			
23	8	2.0	387	H96652			
24	8	2.0	391	1 SYCTK			
25	8	2.0	391	D85558			
26	8	2.0	395	2 A82283			
27	8	2.0	430	E64059			
28	8	2.0	441	2 G82612			
29	2	474	2 B64434				

A; Reference number: Z25014
A; Accession: T49199
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-526 <BEN>
A; Cross-references: EMBL:AL163832; GSPDB:GN00061; ATSP:F27K19.50
A; Gene: ATSP:F27K19.50
A; Map position: 3
C; Superfamily: anthranilate synthase component I
RESULT 4
T50034 anthranilate synthase (EC 4.1.3.27) alpha chain [imported] - Ruta graveolens
C; Species: Ruta graveolens
C; Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
A; Accession: T50034
R; Bohmann, J.; DeLuca, V.; Eillet, U.; Martin, W.
Plant J. 7, 491-501, 1995
A; Title: Purification and cDNA cloning of anthranilate synthase from Ruta graveolens: mc
A; Reference number: Z25253; MUID:95276783
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-613 <BOH>
A; Cross-references: EMBL:L34344; PIDN:AAA74901.1
C; Function: <PBS>
A; Pathway: tryptophan biosynthesis
A; Function: <AAAS>
A; Pathway: biosynthesis of acridone alkaloids
C; Superfamily: anthranilate synthase component I
C; Keywords: carbon-carbon lyase; oxo-acid-lyase

Query Match 2.5%; Score 10; DB 2; Length 526;
Best Local Similarity 100.0%; Pred. No. 0.085; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 362 AGAGIVADS 371
Db 483 AGAGIVADS 492

RESULT 5
A41365 siderophore biosynthetic protein amoA - Aeromonas hydrophila
C; Species: Aeromonas hydrophila
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: A41365
R; Barghouthi, S.; Payne, S.M.; Arceneaux, J.E.L.; Byers, B.R.
J. Bacteriol. 173, 5121-5128, 1991
A; Title: Cloning, mutagenesis, and nucleotide sequence of a siderophore biosynthetic gene
A; Reference number: A40365; MUID:91317731
A; Accession: A40365
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-396 <BAR>
A; Cross-references: GB:M63339
A; Note: the authors cloned the codon GAG for residue 393 as GLY
C; Superfamily: isochorismate synthase

Query Match 2.3%; Score 9; DB 2; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.7; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 360 LFAGAGIVIA 368
Db 358 LFAGAGIVIA 366

RESULT 6
D86116 hypothetical protein menF [imported] - Lactococcus lactis subsp. lactis (strain IL140
C; Species: Lactococcus lactis subsp. lactis
C; Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C; Accession: D86116
R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh
Genome Res. In press, 2001
A; Title: The complete genome sequence of the lactic acid bacterium.
A; Reference number: A86625
A; Accession: D86716
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-404 <STO>
A; Cross-references: GB:AE00176; NID:912723645; PIDN:AAK04830.1; GSPDB:GN00146
A; Experimental source: strain IL1403; MUID:911403
C; Genetics:
A; Gene: menF

Query Match 2.3%; Score 9; DB 2; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.71; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 298 LHPPALGG 305
Db 314 LHPPALGG 322

RESULT 7
B69450 anthranilate synthase component I (trPE) homolog - Archaeoglobus fulgidus
C; Species: Archaeoglobus fulgidus
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Jun-1999
C; Accession: B69450
R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A; Reference number: A69250; MUID:98049343
A; Accession: B69450
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-411 <KLE>
A; Cross-references: GB:AE000992; GB:AF000782; NID:92689315; PIDN:AAB89646.1; PID:9264
C; Superfamily: anthranilate synthase component I

Query Match 2.3%; Score 9; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 0.72; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 362 AGAGIVADS 370
Db 381 AGAGIVADS 389

RESULT 8
T43924 anthranilate synthase component I [imported] - Pyrococcus kodakaraensis

	C;Species: Pyrococcus kodakaraensis C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000 A;Accession: T43924 A;Status: preliminary; translated from GB/EMBL/DBJ A;Molecule type: DNA A;Residues: 1-433 <IM> A;Experimental source: strain KODI A;Cross-references: EMBL:AB030011; PIDN:BA82547.1 A;Gene: trpE C;Genetics: C;Superfamily: anthranilate synthase component I C;Keywords: carbon-carbon lyase; oxo-acid-lyase F;1-462/product: anthranilate synthase component I #status experimental <MAT>
	C;Species: Bacillus subtilis C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000 C;Accession: A69657; S27507; S27508; I39883; T46638; T46639 R;Kunst, F.; Ogasawara, N.; Noszler, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berl, C.; Bron, S.; Bruschi, C.V.; Caldwell, B.; Capriano, S.; Carter, N.M.; Ehrlich, S.D.; Emmerson, P.T.; Errington, J.; Fabret, C.; Ferrari, Nature 350, 249-256, 1997 A;Authors: Fouiliger, D.; Fritz, C.; Fujita, M.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Liech, J., Harwood, C.R.; Heaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; R;anonymous, Genoscope submitted to the EMBL Data Library, July 1999 A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure, reference number: A75001 A;Accession: A75163 A;Status: preliminary A;Residues: 1-434 <RAW> A;Experimental source: strain Orsay C;Genetics: A;Gene: PAB2045 C;Superfamily: anthranilate synthase component I
Query Match	2.3%; Score 9; DB 2; Length 433; Best Local Similarity 100.0%; Pred. No. 0.76; Mismatches 0; Indels 0; Gaps 0;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	362 AGAGIVADS 370 Db 401 AGAGIVADS 409
RESULT	9
R7163	C;Species: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000 C;Accession: A75163 R;anonymous, Genoscope submitted to the EMBL Data Library, July 1999 A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure, reference number: A75001 A;Accession: A75163 A;Status: preliminary A;Residues: 1-434 <RAW> A;Experimental source: strain Orsay C;Genetics: A;Gene: PAB2045 C;Superfamily: anthranilate synthase component I
Query Match	2.3%; Score 9; DB 2; Length 434; Best Local Similarity 100.0%; Pred. No. 0.76; Mismatches 0; Indels 0; Gaps 0;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	362 AGAGIVADS 370 Db 402 AGAGIVADS 410
RESULT	10
R0316	S0316 antranilate synthase (EC 4.1.3.27) component I - Thermus aquaticus C;Species: thermus aquaticus C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 22-Jun-1999 C;Accession: S0316 R;Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T. Biochim. Biophys. Acta 950, 303-312, 1988 A;Bacterial cloning and nucleotide sequence of Thermus thermophilus HB8 trpE and A;Reference number: S0315; MUID:89000781 A;Accession: S0316 A;Molecule type: DNA A;Residues: 1-462 <SAT> A;Cross-references: EMBL:X07744; NID:948261; PIDN:CAA30566.1; PID:948263 A;Note: the source is designated as <i>Thermus thermophilus</i> HB8 A;Note: part of this sequence, including the amino end, was confirmed by protein sequend
	C;Genetics: C;Superfamily: anthranilate synthase component I C;Keywords: menF - Bacillus subtilis F;1-462/product: menF - Bacillus subtilis Query Match 2.3%; Score 9; DB 2; Length 462; Best Local Similarity 100.0%; Pred. No. 0.8; Mismatches 0; Indels 0; Gaps 0; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	362 AGAGIVADS 370 Db 427 AGAGIVADS 435
RESULT	11
A69657	Probable isochorismate synthase (EC 5.4.99.6) menaquinone-specific menF - Bacillus subtilis C;Species: Bacillus subtilis C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000 C;Accession: A69657; S27507; S27508; I39883; T46638; T46639 R;Kunst, F.; Ogasawara, N.; Noszler, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berl, C.; Bron, S.; Bruschi, C.V.; Caldwell, B.; Capriano, S.; Carter, N.M.; Ehrlich, S.D.; Emmerson, P.T.; Errington, J.; Fabret, C.; Ferrari, Nature 350, 249-256, 1997 A;Authors: Fouiliger, D.; Fritz, C.; Fujita, M.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Liech, J., Harwood, C.R.; Heaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; R;anonymous, Genoscope submitted to the EMBL Data Library, July 1999 A;Description: The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtilis</i> , reference number: A69580; MUID:98044033 A;Accession: A69657 A;Status: nucleic acid sequence not shown A;Title: The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtilis</i> , reference number: A69580; MUID:98044033 A;Cross-references: GB:Z99119; GB:AL009126; NID:92635411; PIDN:CAB15061.1; PID:9263551 A;Experimental source: strain 168 R;Rowland, B.; Hill, K.; Mueller, J.; Driscoll, J.; Taber, H. submitted to the EMBL Data Library, October 1991 A;Description: Organization of an operon involved in menaquinone biosynthesis in <i>Bacillus subtilis</i> , reference number: S27507 A;Accession: S27507 A;Molecule type: DNA A;Residues: 1-11 <RAW> A;Cross-references: EMBL:M74538; NID:91185287 A;Accession: S27508 A;Molecule type: DNA A;Residues: 151-471 <RAW> A;Cross-references: EMBL:M74538; NID:91185287 R;Miller, P. J. Bacteriol. 170, 2742-2743, 1988 A;Title: Transcriptional regulation of a promoter in the men gene cluster of <i>Bacillus subtilis</i> A;Accession: I39883 A;Status: translated from GB/EMBL/DBJ A;Molecule type: DNA A;Residues: 1-11 <RAW> A;Cross-references: GB:M21320; NID:9143178; PIDN:AAA22594.1; PID:9551715 R;Bacteriol. 174, 5063-5071, 1992 A;Title: Sequence organization and regulation of the <i>Bacillus subtilis</i> menBE operon. A;Accession: T46638 A;Reference number: A42715; MUID:92332443 A;Status: preliminary; translated from GB/EMBL/DBJ A;Molecule type: DNA A;Residues: 1-11, 'K', 13-110, 'LCYSE', 141-142, 'LL', 'T', 317, 'AKKEVHN', 325, 'T', 32

A;Cross-references: EMBL:M74521; NID:9557486; PIDN:AAA50396.1; PID:9557487
A;Accession: T46639
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Cross-references: EMBL:M74521; NID:9557486; PIDN:AAA50397.1; PID:9557488
A;Residues: 151-471 <DR2>
C;Genetics:
A;Gene: menF
C;Superfamily: isochorismate synthase isomerase
C;Keywords: intramolecular transferase

Query Match 2.3%; Score 9; DB 1; Length 471;
Best Local Similarity 100.0%; Pred. No. 0.82;保守性 0; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12

S71655 anthranilate synthase (EC 4.1.3.27) component I - *Synechocystis* sp. (strain PCC 6803)
N;Intername: protein Sir1979
C;Species: *Synechocystis* sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S71655
R;Kanki, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimojo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-116, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.
A;Reference number: S74322; MUID:97061201
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-485 <KAN>
A;Cross-references: EMBL:D90912; GB:AB001329; NID:91653228; PIDN:BAA18216.1; PID:9165330
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Gene: trPE
A;Start codon: GTG
C;Superfamily: anthranilate synthase component I
C;Keywords: carbon-carbon lyase; oxo-acid-lyase

Query Match 2.3%; Score 9; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 0.84;保守性 0; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13

E70352 anthranilate synthase component I - *Aquifex aeolicus*
C;Species: *Aquifex aeolicus*
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 22-Jun-1999
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V. Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.
A;Reference number: A70300; MUID:98196666
A;Accession: E70352
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-494 <AOE>
A;Cross-references: GB:AE000596; NID:92983196; PIDN:AC05796.1; PID:92983197; GB:AE00055

Query Match 2.3%; Score 9; DB 2; Length 494;
Best Local Similarity 100.0%; Pred. No. 0.85;保守性 0; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14

JX0065 anthranilate synthase (EC 4.1.3.27) component I - *Clostridium thermocellum*
C;Species: *Clostridium thermocellum*
C;Accession: JX0065
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Jun-2000
R;Sato, S.; Nakada, Y.; Honnami, K.; Yasui, K.; Shiratsuchi, A.
J. Biochem. 105, 362-366, 1989
A;Title: Molecular cloning and the nucleotide sequence of the *Clostridium thermocellum* A;Reference number: JX0065; MUID:89278056
A;Accession: JX0065
A;Molecule type: DNA
A;Residues: 1-494 <SAT>
A;Cross-references: GB:D00399; NID:9216420; PIDN:BAA00300.1; PID:9216421
C;Genetics:
A;Gene: trPE
C;Superfamily: anthranilate synthase component I
C;Keywords: carbon-carbon lyase; oxo-acid-lyase

Query Match 2.3%; Score 9; DB 2; Length 494;
Best Local Similarity 100.0%; Pred. No. 0.85;保守性 0; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15

C83857 anthranilate synthase trPE [imported] - *Bacillus halodurans* (strain C-125)
C;Species: *Bacillus halodurans*
C;Accession: C83857
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H Nucleic Acids Res. 28, 4311-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* a A;Reference number: AB3650; MUID:20203314
A;Accession: C83857
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-502 <STO>
A;Cross-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BAB05378.1; GSDB:G A;Experimental source: strain C-125
C;Genetics:
A;Gene: trPE
C;Superfamily: anthranilate synthase component I

Query Match 2.3%; Score 9; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.86;保守性 0; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 16

QY 362 AGAGIVADS 370
Db 458 AGAGIVADS 466

Thu Mar 28 13:30:11 2002

us-08-774-104a-2.oli.rpr

Page 5

Search completed: March 27, 2002, 15:40:00
Job time: 316 sec

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GenCore version 4.5
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ON protein - protein search, using sw modeL

Run on: March 27, 2002, 15:39:39 ; Search time 13.3 Seconds

(without alignments)
1094.431 Million cell updates/sec

Title: US-08-774-104A-2

Perfect score: 397

Sequence: 1 MMTHETRALAQSDLQQLYA.....ETGLKFFPMRQLLKDYNHVE 397

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 100059 seqs, 36664827 residues

Word size : 8

Total number of hits satisfying chosen parameters: 21

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_39; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	10	2.5	511	1 TRPE_STRCO
2	10	2.5	523	1 TRPE_HALVO
3	9	2.3	396	1 AMOA_AERHY
4	9	2.3	411	1 TRPE_ARCFU
5	9	2.3	433	1 TRPE_PYRCU
6	9	2.3	462	1 TRPE_THETH
7	9	2.3	471	1 MENI_BACSU
8	9	2.3	485	1 TRE2_SYN3
9	9	2.3	494	1 TRPE_AQUAE
10	9	2.3	494	1 TRPE_CLOTM
11	9	2.3	508	1 TRPE_BACCA
12	9	2.3	508	1 TRPE_BACST
13	9	2.3	508	1 TRPE_SYN3
14	9	2.3	513	1 TRPE_BACPU
15	9	2.3	515	1 TRPE_BACSU
16	9	2.3	621	1 TRPK_ARATH
17	8	2.0	391	1 ENTC_ECOLI
18	8	2.0	395	1 VIBC_VIBCH
19	8	2.0	403	1 AAT4_ARATH
20	8	2.0	430	1 MENF_HAEIN
21	8	2.0	474	1 TRPE_METUA

Result No.	Score	Query Match Length	DB ID	Description
1	10	2.5	511	1 TRPE_STRCO
2	10	2.5	523	1 TRPE_HALVO
3	9	2.3	396	1 AMOA_AERHY
4	9	2.3	411	1 TRPE_ARCFU
5	9	2.3	433	1 TRPE_PYRCU
6	9	2.3	462	1 TRPE_THETH
7	9	2.3	471	1 MENI_BACSU
8	9	2.3	485	1 TRE2_SYN3
9	9	2.3	494	1 TRPE_AQUAE
10	9	2.3	494	1 TRPE_CLOTM
11	9	2.3	508	1 TRPE_BACCA
12	9	2.3	508	1 TRPE_BACST
13	9	2.3	508	1 TRPE_SYN3
14	9	2.3	513	1 TRPE_BACPU
15	9	2.3	515	1 TRPE_BACSU
16	9	2.3	621	1 TRPK_ARATH
17	8	2.0	391	1 ENTC_ECOLI
18	8	2.0	395	1 VIBC_VIBCH
19	8	2.0	403	1 AAT4_ARATH
20	8	2.0	430	1 MENF_HAEIN
21	8	2.0	474	1 TRPE_METUA

Result No.	Score	Query Match Length	DB ID	Description
1	10	2.5	511	1 TRPE_STRCO
2	10	2.5	523	1 TRPE_HALVO
3	9	2.3	396	1 AMOA_AERHY
4	9	2.3	411	1 TRPE_ARCFU
5	9	2.3	433	1 TRPE_PYRCU
6	9	2.3	462	1 TRPE_THETH
7	9	2.3	471	1 MENI_BACSU
8	9	2.3	485	1 TRE2_SYN3
9	9	2.3	494	1 TRPE_AQUAE
10	9	2.3	494	1 TRPE_CLOTM
11	9	2.3	508	1 TRPE_BACCA
12	9	2.3	508	1 TRPE_BACST
13	9	2.3	508	1 TRPE_SYN3
14	9	2.3	513	1 TRPE_BACPU
15	9	2.3	515	1 TRPE_BACSU
16	9	2.3	621	1 TRPK_ARATH
17	8	2.0	391	1 ENTC_ECOLI
18	8	2.0	395	1 VIBC_VIBCH
19	8	2.0	403	1 AAT4_ARATH
20	8	2.0	430	1 MENF_HAEIN
21	8	2.0	474	1 TRPE_METUA

Result No.	Score	Query Match Length	DB ID	Description
1	10	2.5	511	1 TRPE_STRCO
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14	9	2.3	513	1 TRPE_BACPU
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8	9	2.3	485	1 TRE2_SYN3

-!- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY SIMILARITY).

-!- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES GLUTAMINE AMIDOTRANSFERASE ACTIVITY.

-!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I FAMILY.

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CC EMBL; M83788; AAA73177.1; -

CC PIR; A42301; A42301; -

CC DR InterPro; IPR00350; Chorismate_bind.

CC DR Pfam; PF00425; chorismate_bind; 1.

CC DR Prodom; PDO0779; Chorismate_bind; 1.

CC KW Isomerase; Iron transport.

CC SQ SEQUENCE; 396 AA; 42074 MW; 5361F4C18EEFAE9D CRC64;

Query Match 2.5%; Score 10; DB 1; Length 523;

Best Local Similarity 100.0%; Pred. No. 0.035; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR PRINTS; PR0005; ANTSNTHASEI.

DR PROBON; PD000779; Chorismate_bind; 1.

DR TRYPTOPHAN biosynthesis; Lyase.

SQ SEQUENCE 523 AA; 55920 MW; 9765667997636A6C CRC64;

Query Match 2.3%; Score 9; DB 1; Length 395;

Best Local Similarity 100.0%; Pred. No. 0.3; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR PRINTS; PR0005; ANTSNTHASEI.

DR PROBON; PD000779; Chorismate_bind; 1.

DR TRYPTOPHAN biosynthesis; Lyase.

SQ SEQUENCE 358 LFAGAGIVAA 366

RESULT 4

ID TRPE_ARCFU STANDARD; PRT: 411 AA.

ID TRPE_ARCFU STANDARD; PRT: 411 AA.

AC 028669; -

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).

GN TRPE OR AFG603.

OS Archaeoglobus fulgidus.

OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;

OX NCBI_TaxID=2234;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=VC-16 / DSM 4304 / ATCC 4955B;

RX MEDLINE=98049343; PubMed=9389475;

RA Kleck H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Retchum K.A., Dodson R.J., Gwynn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.D., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., Neiland L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaline B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.", Nature 390:364-370(1997).

NCBI_TAXID=644;

RN [1]

RC SEQUENCE FROM N.A.

RC STRAIN=95A2;

RX MEDLINE=1317731; PubMed=1830579;

RA Bargouthi S., Payne S.M., Arceneaux J.E., Byers B.R.; "Cloning, mutagenesis, and nucleotide sequence of a siderophore biosynthetic gene (amoA) from Aeromonas hydrophila.", RT J. Bacteriol. 173:5121-5128(1991).

RT J. Bacteriol. 173:5121-5128(1991).

RC -!- PATHWAY: AMONABACTIN BIOSYNTHESIS. AMONABACTIN IS AN IRON-CHELATING COMPOUND INVOLVED IN TRANSPORTING IRON FROM THE BACTERIAL ENVIRONMENT INTO THE CELL CYTOPLASM.

CC -!- SIMILARITY: STRONG, TO OTHER ISOCHORISMATE SYNTHASES; WEAK, TO TROPIC AND PABB.

CC -!- CATALYTIC ACTIVITY: CHORISMATE = ISOCHORISMATE.

CC -!- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY SIMILARITY).

CC -!- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES GLUTAMINE AMIDOTRANSFERASE ACTIVITY.

CC -!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I FAMILY.

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CC EMBL; AE000992; AAB89646.1; -

CC TIGR; AF1603; -

CC InterPro; IPR00350; Chorismate_bind.

CC DR Pfam; PF00425; chorismate_bind; 1.

CC DR PRINTS; PR0005; ANTSNTHASEI.

CC DR PROBON; PD000779; Chorismate_bind; 1.

CC DR TRYPTOPHAN biosynthesis; Lyase.

DR TIGR; AF1603; -

DR InterPro; IPR00350; Chorismate_bind.

DR Pfam; PF00425; chorismate_bind; 1.

DR PRINTS; PR0005; ANTSNTHASEI.

DR PROBON; PD000779; Chorismate_bind; 1.

DR TRYPTOPHAN biosynthesis; Lyase.

KW EMBL; M83339; AAA71935.1; -

DR PIR; A40365; A40365.

RP : aeolicus.;"
 RL : Nature 392:353-358(1998).
 CC : -!- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE +
 CC : PYRUVATE + L-GLUTAMATE
 CC : -!- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
 CC : -!- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY
 CC : SIMILARITY).
 CC : -!- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
 CC : USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
 CC : GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
 CC : -!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
 CC : FAMILY.
 CC :
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 CC : or send an email to license@isb-sib.ch).
 DR : EMBL; D00399; BAQ0300_1; -
 DR : PIR; JX0065; JX0065.
 DR : InterPro; IPK00350; Chorismate_bind.
 DR : Pfam; PF0425; chorismate_bind; 1.
 DR : PRINTS; PR00095; ANTSWHAESI.
 DR : PRODOM; PD000779; Chorismate_bind; 1.
 DR : KWR : TRYptophan biosynthesis; Lyase.
 DR : SEQUENCE 494 AA; 56020 MW; 32DF1E2234447D CRC64;
 DR :
 DR : PRINTS; PR00095; ANTSWHAESI.
 DR : PRODOM; PD000779; Chorismate_bind; 1.
 DR : Pfam; PF0425; chorismate_bind; 1.
 DR : InterPro; IPR0005350; Chorismate_bind.
 DR :
 DR : PIR; JX0065; JX0065.
 DR : InterPro; IPK00350; Chorismate_bind.
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 DR : InterPro; IPK00350; Chorismate_bind.
 DR : Pfam; PF0425; chorismate_bind; 1.
 DR : PRINTS; PR00095; ANTSWHAESI.
 DR : PRODOM; PD000779; Chorismate_bind; 1.
 DR : KWR : TRYptophan biosynthesis; Lyase.
 DR : SEQUENCE 508 AA; 56492 MW; 3DA113D811A77797 CRC64;
 DR :
 DR : PRINTS; PR00095; ANTSWHAESI.
 DR : PRODOM; PD000779; Chorismate_bind; 1.
 DR : Pfam; PF0425; chorismate_bind; 1.
 DR : InterPro; IPR0005350; Chorismate_bind.
 DR :
 DR : PIR; JX0065; JX0065.
 DR : InterPro; IPK00350; Chorismate_bind.
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 DR : PIR; JX0065; JX0065.
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 DR : PRODOM; PD000779; Chorismate_bind; 1.
 DR : KWR : TRYptophan biosynthesis; Lyase.
 DR : SEQUENCE 508 AA; 56492 MW; 3DA113D811A77797 CRC64;

Query Match 2.3%; Score 9; DB 1; Length 508;
 Best Local Similarity 100.0%; Pred. No. 0.37; O; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 362 AGAGIVADS 370
 Db 465 AGAGIVADS 473

RESULT 12

ID TRPE_BACST STANDARD: PRN: 508 AA.

TRPE_BACST 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
 DE GN TRPE.
 OS Bacillus stearothermophilus
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Geobacillus.
 OX NCBI_TaxID=1422;

RN [1] RQ SEQUENCE FROM N.A.
 RP STRAIN=TCC 12980 / NCA 26;
 RX MEDLINE=9929394; PubMed=10369778;
 RA Chen X.-P., Antson A.A., Yang M., Baumann C., Dodson E.J.,
 RA Dodson G.G., Golnick P.;
 RT "Regulatory features of the trp operon and the crystal structure of
 RT the trp RNA-binding attenuation protein from *Bacillus*
 RT *stearothermophilus*";
 RL J. Mol. Biol. 289:1003-1016(1999).
 CC -I- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE +
 PYRUVATE + L-GLUTAMATE.
 CC -I- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
 CC -I- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY
 SIMILARITY).
 CC -I- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE
 USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES
 GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
 CC -I- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
 FAMILY.
 CC

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CC

EMBL: AF139834; AAP33791.1; -
 DR InterPro: IPR000350; Chorismate_bind.
 DR PRINTS: PR0045; chorismate_bind; 1.
 DR PRODOM: PD000779; Chorismate_bind; 1.
 KW tryptophan biosynthesis; Lyase.
 SQ SEQUENCE 508 AA; 56440 MW; 25EB252616160ADD CRC64;

Query Match 2.3%; Score 9; DB 1; Length 508;
 Best Local Similarity 100.0%; Pred. No. 0.37; O; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 362 AGAGIVADS 370
 Db 465 AGAGIVADS 473

RESULT 13

ID TRPE_SYN3 STANDARD: PRN: 508 AA.

TRPE_SYN3 09x6j4; 01-Nov-1997 (Rel. 35, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE PROBABLE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
 DE TRPE OR SLR0738.
 OS *Synechocystis* sp. (strain RCC 6803);
 OC Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;

RN [1] RQ SEQUENCE FROM N.A.
 RP MEDLINE=97061201; PubMed=8905231;
 RX RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hiroseawa M., Sugiyama S., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nario K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.", DNA Res. 3:109-136(1996).
 RN [2] RQ SEQUENCE OF 1-408 FROM N.A.
 RP MEDLINE=89034300; PubMed=3141423;
 RX RA Reilly P., Humes J.D., Pan Y.C.E., Nelson N.;
 RT RT "Molecular cloning and sequencing of the psad gene encoding subunit II of photosystem I from the cyanobacterium, *Synechocystis* sp. PCC 6803.", J. Biol. Chem. 263:17658-17662(1988).
 CC CC -I- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE + PYRUVATE + L-GLUTAMATE.
 CC CC -I- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
 CC CC -I- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY SIMILARITY).
 CC CC -I- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
 CC CC -I- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I FAMILY.
 CC CC -I- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 182.
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 CC DR EMBL: D90899; BAA16689_1; -
 DR EMBL: J04195; AAAB8626_1; ALT_FRAME.
 DR EMBL: J04195; AAAB8627_1; ALT_FRAME.
 DR PIR: B33124; B32124.
 DR PIR: C32124; C32124.
 DR InterPro: IPR000350; chorismate_bind.
 DR Pfam: PF00425; chorismate_bind; 1.
 DR PRINTS: PR00095; ANTSNTHASE.
 DR PRODOM: PD000779; Chorismate_bind; 1.
 KW tryptophan biosynthesis; Lyase; Complete proteome.
 SQ SEQUENCE 508 AA; 57147 MW; A3308E9A7B8A1FC1 CRC64;

Query Match 2.3%; Score 9; DB 1; Length 508;
 Best Local Similarity 100.0%; Pred. No. 0.37; O; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 363 GAGIVADS 371
 Db 477 GAGIVADS 485

RESULT 14

TRP_E_BACPU STANDARD; PRT; 513 AA.
 ID TRP_E_BACPU STANDARD;
 AC P18267;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
 OC Bacillus pumilus (Bacillus mesentericus).
 OS Bacteria; Firmicutes; Bacillus/clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TAXID=1408;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=RUB502;
 RX MEDLINE=90236301; PubMed=2110100;
 RA Rivas M.V., Jarvis E.D., Rodner R.;
 RT "the structure of the trpe, trpp and 5' trpc genes of *Bacillus pumilus*";
 RT Gene 87:71-78(1990).
 [2]
 RPERRATUM
 RX MEDLINE=91033058; PubMed=2227447;
 RA Rivas M.V., Jarvis E.D., Rodner R.;
 RL Gene 94:141-143(1990).
 CC -!- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE + PYRUVATE + L-GLUTAMATE.
 CC -!- PATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
 CC -!- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY SIMILARITY).
 CC -!- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF ANTHRANILATE USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
 CC -!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I FAMILY.
 CC
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 CC
 CC -!- POSITION: REF.2 AND REF.3 SEQUENCES DIFFER FROM THAT SHOWN IN POSITIONS 343 TO 402 DUE TO A FRAMESHIFT.
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 CC
 CC -!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I FAMILY.
 CC -!- CAUTION: REF.2 AND REF.3 SEQUENCES DIFFER FROM THAT SHOWN IN POSITIONS 343 TO 402 DUE TO A FRAMESHIFT.
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 CC
 DR PIR: JH0098; JH0098.
 DR InterPro: IPR000550; Chorismate_bind.
 DR Pfam: PF00475; chorismate_bind; 1.
 DR ProDom: PD000779; Chorismate_bind; 1.
 DR KW Tryptophan biosynthesis; Lyase.
 SQ SEQUENCE 513 AA; 58091 MW; 0E6B19904421CC5A CRC64;

Query Match 2.3%; Score 9; DB 1; Length 513;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADS 370
 DB 462 AGAGIVADS 470

RESULT 15
 ID TRP_E_BACSU STANDARD; PRT; 515 AA.
 AC P03963;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
 TRP_E_BACSU STANDARD; PRT; 515 AA.
 ID TRP_E_BACSU STANDARD; PRT; 515 AA.
 AC P03963;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.27).
 OC Bacillus subtilis.

Query Match 2.3%; Score 9; DB 1; Length 515;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 AGAGIVADS 370
 DB 464 AGAGIVADS 472

OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TAXID=1423;
 RN [1] SEQUENCE FROM N.A.
 RP Hennер D.J.;
 RA "Sequence of *Bacillus subtilis* gbpA, mtr(A,B), gerc(1-3), ndk, cher, arc(B,E,F,H), trpA-F, hisH, and tyra genes.",
 RT Submitted (ANN-1992) to the EMBL/GenBank/DDBJ databases.
 RN [2] PRELIMINARY SEQUENCE FROM N.A.
 RP MEDLINE=8523062; PubMed=394737;
 RX Hennér D.J., Band L., Shimotsu H.;
 RT "Nucleotide sequence of the *Bacillus subtilis* tryptophan operon.";
 RL Gene 34:169-177(1985).
 RN [3] PRELIMINARY SEQUENCE FROM N.A.
 RP MEDLINE=84183611; PubMed=645119;
 RX Band L., Shimotsu H., Hennér D.J.;
 RA "Nucleotide sequence of the *Bacillus subtilis* trpE and trpD genes.";
 RL Gene 27:55-65(1984).
 RN [4] SEQUENCE OF 1-40 FROM N.A.
 RP MEDLINE=8503507; PubMed=6436812;
 RX Shinotsu H., Hennér D.J.;
 RT "Characterization of the *Bacillus subtilis* tryptophan promoter region.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:6315-6319(1984).
 CC -!- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE = ANTHRANILATE + PYRUVATE + L-GLUTAMATE.
 CC -!- PYRUVATE + L-GLUTAMATE.
 CC -!- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY SIMILARITY).
 CC -!- MISCELLANEOUS: COMPONENT I CATALYZES THE FORMATION OF TRYPTOPHAN USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS COMPONENT II PROVIDES GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
 CC -!- SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I FAMILY.
 CC -!- POSITION: REF.2 AND REF.3 SEQUENCES DIFFER FROM THAT SHOWN IN POSITIONS 343 TO 402 DUE TO A FRAMESHIFT.
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 CC
 DR EMBL; M36468; AAB02272; 1; ALT_INIT.
 DR PIR: JH0098; JH0098.
 DR InterPro: IPR000550; Chorismate_bind.
 DR Pfam: PF00475; chorismate_bind; 1.
 DR ProDom: PD000779; Chorismate_bind; 1.
 DR EMBL; M00245; AAA20862; 1; -.
 DR EMBL; K01391; AAA22865; 1; -.
 DR EMBL; M27566; AAA22875; 1; -.
 DR EMBL; Z99115; CAB14184; 1; -.
 DR PIR: A01119; NBBS1.
 DR PIR: A22063; A22063.
 DR PIR: A22794; A22794.
 DR Subcellist; B3J0287; trpE.
 DR InterPro: IPR000350; Chorismate_bind.
 DR Pfam: PF00475; chorismate_bind; 1.
 DR PRINTS; PR00095; ANTSNTHASEI.
 DR ProDom: PD000779; Chorismate_bind; 1.
 DR PDB; PDB00000000; Chorismate_bind; 1.
 DR KW Tryptophan biosynthesis; Lyase; Complete proteome.
 FT CONFLICT 80 120 120 A -> S (IN REF. 2 AND 3).
 FT SEQUENCE 515 AA; 58016 MW; 33B88D9D80B0CD991 CRC64;

Thu Mar 28 13:30:11 2002

us-08-774-104a-2.ol.i.rsp

Search completed: March 27, 2002, 15:43:04
Job time: 205 sec

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Q9Pby0 xylella fas
Q81533 nicotiana t
Q9be73 macaca fasc

OM protein - protein search, using sw model

Run on:

March 27, 2002, 15:39:09 ; Search time 25.43 Seconds

(without alignments)
2283.528 Million cell updates/sec

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description	RESULT	1
1	339	85.4	398	4 Q9UA3	Q9UA3	PRELIMINARY; PRM; 398 AA.
2	10	2.5	524	2 Q9A490	Q9UA3;	AC
3	10	2.5	526	2 Q9LY58	Q9UA3;	DT 01-MAY-2000 (TREMBLrel. 13, Created)
4	10	2.5	608	10 Q41155	Q9UA3;	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
5	10	2.5	608	10 Q9AW5	Q9UA3;	DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
6	10	2.5	613	10 Q41156	Q9UA3;	DE NEUTRAL SPHINGOMELINASE.
7	9	2.3	404	2 Q9CHJ9	Q9UA3;	OS Homo sapiens (Human).
8	9	2.3	434	1 Q9TIG5	Q9UA3;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
9	9	2.3	453	2 Q99V51	Q9UA3;	OC Mammalia; Eutheria; Primates; Cattarrhini; Hominidae; Homo.
10	9	2.3	502	2 Q9KCB4	Q9UA3;	OX NCBI_TAXID=9606;
11	9	2.3	577	10 Q9XJ30	Q9UA3;	RN [1]
12	9	2.3	606	10 Q9XJ29	Q9UA3;	RP SPROT FROM N.A.
13	8	2.0	55	2 Q9AP3	Q9UA3;	RC TISSUE-KIDNEY;
14	8	2.0	141	2 Q9I166	Q9UA3;	RX Chatterjee S, Han H, Rollins S, Cleveland T, RT "Molecular cloning, characterization, and expression of a novel human
15	8	2.0	387	10 Q9S169	Q9UA3;	RT neutral sphingomyelinase.", RL J. Biol. Chem. 274:37407-37412(1999).
16	8	2.0	391	2 P95475	Q9UA3;	DR EML1; AF069140; AAF19052.1, -
17	8	2.0	408	2 Q9E639	Q9UA3;	DR InterPro: IPR000050; Chorismate bind.
18	8	2.0	427	2 Q9RZB0	Q9UA3;	DR Pfam: PF00425; chorismate_bind; 1.
19	8	2.0	436	4 Q9H8R2	Q9UA3;	DR PRINTS; PRO00095; ANTSWIMASEL.
					Db PRODOM; PD000779; Chorismate.bind; 1.	SQ SEQUENCE 398 AA; 43590 MW; 0248D89974C77BC1 CRC64;
					Query Match 85.4%; Score 339; DB 4; Length 398;	
					Best Local Similarity 100.0%; Pred. No. 0; MisMatches 0; Indels 0; Gaps 0;	
					Matches 339; Conservative 0; Mismatches 0;	
					QY 59 VRGAQSDFEQEPPOSELMAGNEFWNPENVTIAADKTFGSDTWSDFTTWLAQFVPKOPTN 118	
					Db 60 VIGAQSFDEQEPOSELMAGNEFWNPENVTIAADKTFGSDTWSDFTTWLAQFVPKOPTN 119	
					QY 119 VTMISHVNTDEVWERTLENLDTLAIOTLAKYVGRQOTLQLDQTLLAQITRALAQAN 178	
					Db 120 VTMISHVNTDEVWERTLENLDTLAIOTLAKYVGRQOTLQLDQTLLAQITRALAQAN 179	
					QY 179 TYHVWLRKRHDELTISATPVERUAMSGQIATAVAGTSRRGTDGADDIALGEALLSQKN 238	
					Db 180 TYHVWLRKRHDELTISATPVERUAMSGQIATAVAGTSRRGTDGADDIALGEALLSQKN 239	
					QY 239 RIEHQYVVAISITRLQDVTTSLKPAMPSSLNLKKQVQHLYTRITGDIAHLSTVATVDR 298	
					Db 240 RIEHQYVVAISITRLQDVTTSLKPAMPSSLNLKKQVQHLYTRITGDIAHLSTVATVDR 299	
					QY 299 HPPPALEGCPVPREALYYIATHEKTPRGFLFAGPIGFYPTADNSCEFWVGIRSMVNQTORRA 358	
					Db 300 HPPPALEGCPVPREALYYIATHEKTPRGFLFAGPIGFYPTADNSCEFWVGIRSMVNQTORRA 359	
					QY 359 TLEFAGCIVADSQAEYEETSGIKFPEMRQLKDYNHE 397	
					Db 360 TLFAGCIVADSQAEYEETSGIKFPEMRQLKDYNHE 398	
					RESULT 2	
					Q9R490	
					ID Q9R490	PRELIMINARY; PRM; 524 AA.
					AC Q9R490;	
					DT 01-JUN-2001 (TREMBLrel. 17, Created)	
					DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)	
					DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)	
					DE PARA-AMINOBENZOATE SYNTHASE, COMPONENT I.	

GN	CC2953.					
OS	Caulobacter crescentus					
OC	Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;					
OC	Caulobacter.					
OX	NCBI_TAXID:69394;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	Medline+21173698; Pubmed=112259647;					
RA	Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J.J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haff D.H., Kolonay J.F., Smits J.J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Yamashita J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001); TIGR; CC2953; -.					
RL	Complete genome sequence of Caulobacter crescentus ";					
DR	EMBL; AE005959; AAC24915.1; -.					
KW	complete proteome;					
SQ	SEQUENCE 524 AA; 5526 MW; 680D4B427AAAD5D CRC64;					
Query Match	2.5%; Score 10; DB 2; Length 524;					
Best Local Similarity	100.0%; Pred. No. 0; 26; Mismatches 0; Indels 0; Gaps 0;					
Matches	10; Conservative					
QY	362 AGAGIVADSD 371					
DB	494 AGAGIVADSD 503					
RESULT	3					
ID	O9LY58	PRELIMINARY;	PRT;	526 AA.		
AC	O9LY58					
DT	01-OCT-2000 (TREMBLrel. 15, Created)					
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)					
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)					
DE	ANTHRANILATE SYNTHASE ALPHA-1 CHAIN-LIKE PROTEIN.					
GN	F27K19_5.0					
OS	Arabidopsis thaliana (Mouse-ear cress); Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.					
OC	OC					
OC	eurosids II; Brassicales; Brassicaceae; Arabidopsis.					
NCBI_TAXID:3702;						
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	Benes V., Wurmback E., Drzeneck H., Ausurge W., Newes H.W., Rudd S., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.					
RL	[2]					
RN	SBQUENCE FROM N.A.					
RA	EU Arabidopsis sequencing project; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.					
RL	EMBL; AL163032; CAB8741.1; -.					
DR	InterPro; IPR000350; Chorismate_bind.					
PRMT	PF00425; chorismate_bind.					
DR	Prodrom; PR00095; ANTSNTHAS1.					
DR	SEQUENCE 526 AA; 59296 MW; AB4DAFD4AA73986C CRC64;					
Query Match	2.5%; Score 10; DB 10; Length 526;					
Best Local Similarity	100.0%; Pred. No. 0; 26; Mismatches 0; Indels 0; Gaps 0;					
Matches	10; Conservative					
QY	362 AGAGIVADSD 371					
DB	483 AGAGIVADSD 492					
RESULT	4					
Query Match	2.5%; Score 10; DB 10; Length 608;					
Best Local Similarity	100.0%; Pred. No. 0; 3; Mismatches 0; Indels 0; Gaps 0;					
Matches	10; Conservative					
Q41155	SEQUENCE FROM N.A.	PRELIMINARY;	PRT;	608 AA.		
ID	Q41155					
AC	Q41155;					
DT	01-NOV-1996 (TREMBLrel. 01, Created)					
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)					
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)					
DE	ANTHRANILATE SYNTHASE ALPHA SUBUNIT PRECURSOR.					
OS	Ruta graveolens (common rue).					
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids II; Sapindales; Rutaceae; Ruta.					
OC	eurosids II; Sapindales; Rutaceae; Ruta.					
NCBI_TAXID:37565;						
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	Medline+95276783; Pubmed=7757119;					
RA	Boilmann J., DeLuca V., Elert U., Martin W.; Purification and cloning of anthranilate synthase from Ruta graveolens: modes of expression and properties of native and recombinant enzymes. ";					
RT	RL Plant J 7:491-501(1995); Plant; PR00425; chorismate_bind; 1.					
DR	EMBL; L33434; AAA74900.1; -.					
DR	HSSP; Q06128; 1QDL.					
DR	Mendel; 12275; Rotgr;433;12275.					
DR	InterPro; IPR003550; Chorismate_bind.					
DR	PRMT; PR00425; chorismate_bind; 1.					
DR	Prodrom; PD000779; Chorismate_bind; 1.					
KW	Signal.					
FT	SIGNAL 1 89					
CHIN	90 608					
FT	POTENTIAL.					
SEQUENCE	608 AA; 67992 MW; 40F7DB56F49366A5 CRC64;					
Query Match	2.5%; Score 10; DB 10; Length 608;					
Best Local Similarity	100.0%; Pred. No. 0; 3; Mismatches 0; Indels 0; Gaps 0;					
Matches	10; Conservative					
QY	362 AGAGIVADSD 371					
DB	570 AGAGIVADSD 579					
RESULT	5					
ID	Q9AW95	PRELIMINARY;	PRT;	608 AA.		
AC	Q9AW95;					
DT	01-JUN-2001 (TREMBLrel. 17, Created)					
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)					
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)					
DE	ANTHRANILATE SYNTHASE ALPHA SUBUNIT (EC 4.1.3.27).					
GN	ASA.					
OS	Catharanthus roseus (Rose periwinkle) (Madagascar periwinkle).					
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; Asteridae; eudicots 1; Gentianales; Apocynaceae; Catharanthus.					
OC	Asteridae; eudicots 1; Gentianales; Apocynaceae; Catharanthus.					
NCBI_TAXID:4058;						
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	STRAIN=; DON; TISSUE=CELL SUSPENSION;					
RA	Bongaerts R.J.M., Meijer A.H., Verpoorte R.; Molecular cloning and characterization of a cDNA clone encoding the alpha-subunit of the enzyme anthranilate synthase from Catharanthus roseus. ";					
RA	Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.					
DR	EMBL; AU250008; CAC29060.1; -.					
KW	Livase.					
SQ	SEQUENCE 608 AA; 68263 MW; DEB052CE5A1FC15E CRC64;					
Query Match	2.5%; Score 10; DB 10; Length 608;					
Best Local Similarity	100.0%; Pred. No. 0; 3; Mismatches 0; Indels 0; Gaps 0;					
Matches	10; Conservative					
QY	362 AGAGIVADSD 371					
DB	483 AGAGIVADSD 492					

QY	362 AGAGIVADS 371	KW	Complete proteome.
ID	Q41156	SEQUENCE	404 AA; 46450 MW; 83BFC659F45AB060 CRC64;
AC	Q41156;	PRT;	613 AA.
DT	01-NOV-1996 (TREMBREL. 01, Created)	Query Match	2.3%; Score 9; DB 2; Length 404;
DE	01-NOV-1996 (TREMBREL. 01, Last sequence update)	Best local Similarity	100.0%; Pred. No. 2.1; Mismatches 0; Indels 0; Gaps 0;
DT	01-JUN-2001 (TREMBREL. 17, Last annotation update)	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DE	ANTHRANILATE SYNTHASE ALPHA SUBUNIT PRECURSOR.	AC	Q9VIG5;
OS	Ruta graveolens (common rue).	ID	Q9VIG5;
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	PRT;	434 AA.
OC	Spermatophyta; Magnoliophyta; eudicots; Rosidae;	Query Match	2.3%; Score 9; DB 2; Length 404;
RT	eurosidia II; Sapindales; Rutaceae; Ruta.	Best local Similarity	100.0%; Pred. No. 2.1; Mismatches 0; Indels 0; Gaps 0;
OX	[1]	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RN	SEQUENCE FROM N.A.	AC	Q9VIG5;
RP	MEDLINE:95276783; PubMed:7757119;	ID	Q9VIG5;
RA	Bohlmann J., DeLucia V., Eilert U., Martin W.;	PRT;	434 AA.
RT	*Purification and cDNA cloning of anthranilate synthase from Ruta graveolens: modes of expression and properties of native and recombinant enzymes.;	Query Match	2.3%; Score 9; DB 2; Length 404;
PL	Plant J. 7:491-501(1995).	Best local Similarity	100.0%; Pred. No. 2.1; Mismatches 0; Indels 0; Gaps 0;
EMBL	U34344; AA74901.1; -.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	HSSP; Q06128; 1QDL.	AC	Q9VIG5;
DR	Mendel; 12216; Rngr;r1433;12276.	ID	Q9VIG5;
DR	InterPro; IPR000350; Chorismate_bind.	PRT;	434 AA.
DR	PRINTS; PRO0095; ANTSNTHASEI.	Query Match	2.3%; Score 9; DB 2; Length 404;
DR	ProDom; PD000779; Chorismate_bind; 1.	Best local Similarity	100.0%; Pred. No. 2.1; Mismatches 0; Indels 0; Gaps 0;
KW	Signal.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT	SIGNAL 1 92 POTENTIAL.	AC	Q9VIG5;
FT	CHAIN 93 613 AA; 67918 MW; 9986339474ABFF75 CRC64;	ID	Q9VIG5;
SQ	SEQUENCE	PRT;	434 AA.
QY	362 AGAGIVADS 371	Query Match	2.3%; Score 9; DB 1; Length 434;
DB	572 AGAGIVADS 581	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
RESULT	7	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Q9CHJ9	PRELIMINARY;	AC	Q9CHJ9;
ID	Q9CHJ9	PRT;	404 AA.
AC	Q9CHJ9;	Query Match	2.3%; Score 9; DB 1; Length 434;
DT	01-JUN-2001 (TREMBREL. 17, Created)	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DE	01-JUN-2001 (TREMBREL. 17, Last sequence update)	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
GN	MEMBRANE-SPECIFIC ISOCHORISMATE SYNTHASE (EC 5.4.99.6).	AC	Q9VIG5;
OS	Lactococcus lactis (subsp. lactis) (Streptococcus lactis).	ID	Q9VIG5;
OC	Bacteria; Firmicutes; Bacilli/Clostridium group; Streptococcaceae; Lactococcus.	PRT;	434 AA.
OC	NCBL_TaxID=1360;	Query Match	2.3%; Score 9; DB 1; Length 434;
RN	[1]	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
RP	SEQUENCE FROM N.A.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RC	STRAIN="TL1403;"	AC	Q9VIG5;
RA	Weissenbach J., Wincker P., Manger S., Jaillon O., Malarme K., Bolotin A., Wincker P., Manger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.;	ID	Q9VIG5;
RT	"the complete genome sequence of the lactic acid bacterium Lactococcus lactis.", Genome Res. 0:0-0(2001).	PRT;	453 AA.
DR	EMBL; AB006306; DAK04330.1; -.	Query Match	2.3%; Score 9; DB 1; Length 434;
DR	InterPro; IPR000350; Chorismate_bind.	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DR	InterPro; IPR00425; Chorismate_bind; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	AC	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	ID	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	PRT;	402 AGAGIVADS 410
RESULT	7	Query Match	2.3%; Score 9; DB 1; Length 434;
Q9CHJ9	PRELIMINARY;	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
ID	Q9CHJ9	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AC	Q9CHJ9;	AC	Q9VIG5;
DT	01-JUN-2001 (TREMBREL. 17, Last annotation update)	ID	Q9VIG5;
DE	MEMBRANE-SPECIFIC ISOCHORISMATE SYNTHASE (EC 5.4.99.6).	PRT;	453 AA.
GN	01-JUN-2001 (TREMBREL. 17, Last sequence update)	Query Match	2.3%; Score 9; DB 1; Length 434;
OS	Lactococcus lactis (subsp. lactis) (Streptococcus lactis).	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
OC	Bacteria; Firmicutes; Bacilli/Clostridium group; Streptococcaceae; Lactococcus.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OC	NCBL_TaxID=1360;	AC	Q9VIG5;
RN	[1]	ID	Q9VIG5;
RP	SEQUENCE FROM N.A.	PRT;	453 AA.
RC	STRAIN="TL1403;"	Query Match	2.3%; Score 9; DB 1; Length 434;
RA	Weissenbach J., Wincker P., Manger S., Jaillon O., Malarme K., Bolotin A., Wincker P., Manger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.;	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
RT	"the complete genome sequence of the lactic acid bacterium Lactococcus lactis.", Genome Res. 0:0-0(2001).	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	EMBL; AB006306; DAK04330.1; -.	AC	Q9VIG5;
DR	InterPro; IPR000350; Chorismate_bind.	ID	Q9VIG5;
DR	InterPro; IPR00425; Chorismate_bind; 1.	PRT;	453 AA.
DR	ProDom; PD000779; Chorismate_bind; 1.	Query Match	2.3%; Score 9; DB 1; Length 434;
DR	ProDom; PD000779; Chorismate_bind; 1.	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	AC	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	ID	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	PRT;	453 AA.
DR	ProDom; PD000779; Chorismate_bind; 1.	Query Match	2.3%; Score 9; DB 1; Length 434;
DR	ProDom; PD000779; Chorismate_bind; 1.	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	AC	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	ID	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	PRT;	453 AA.
DR	ProDom; PD000779; Chorismate_bind; 1.	Query Match	2.3%; Score 9; DB 1; Length 434;
DR	ProDom; PD000779; Chorismate_bind; 1.	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	AC	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	ID	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	PRT;	453 AA.
DR	ProDom; PD000779; Chorismate_bind; 1.	Query Match	2.3%; Score 9; DB 1; Length 434;
DR	ProDom; PD000779; Chorismate_bind; 1.	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	AC	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	ID	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	PRT;	453 AA.
DR	ProDom; PD000779; Chorismate_bind; 1.	Query Match	2.3%; Score 9; DB 1; Length 434;
DR	ProDom; PD000779; Chorismate_bind; 1.	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	AC	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	ID	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	PRT;	453 AA.
DR	ProDom; PD000779; Chorismate_bind; 1.	Query Match	2.3%; Score 9; DB 1; Length 434;
DR	ProDom; PD000779; Chorismate_bind; 1.	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	AC	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	ID	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	PRT;	453 AA.
DR	ProDom; PD000779; Chorismate_bind; 1.	Query Match	2.3%; Score 9; DB 1; Length 434;
DR	ProDom; PD000779; Chorismate_bind; 1.	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	AC	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	ID	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	PRT;	453 AA.
DR	ProDom; PD000779; Chorismate_bind; 1.	Query Match	2.3%; Score 9; DB 1; Length 434;
DR	ProDom; PD000779; Chorismate_bind; 1.	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	AC	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	ID	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	PRT;	453 AA.
DR	ProDom; PD000779; Chorismate_bind; 1.	Query Match	2.3%; Score 9; DB 1; Length 434;
DR	ProDom; PD000779; Chorismate_bind; 1.	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	AC	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	ID	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	PRT;	453 AA.
DR	ProDom; PD000779; Chorismate_bind; 1.	Query Match	2.3%; Score 9; DB 1; Length 434;
DR	ProDom; PD000779; Chorismate_bind; 1.	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	AC	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	ID	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	PRT;	453 AA.
DR	ProDom; PD000779; Chorismate_bind; 1.	Query Match	2.3%; Score 9; DB 1; Length 434;
DR	ProDom; PD000779; Chorismate_bind; 1.	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	AC	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	ID	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	PRT;	453 AA.
DR	ProDom; PD000779; Chorismate_bind; 1.	Query Match	2.3%; Score 9; DB 1; Length 434;
DR	ProDom; PD000779; Chorismate_bind; 1.	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	AC	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	ID	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	PRT;	453 AA.
DR	ProDom; PD000779; Chorismate_bind; 1.	Query Match	2.3%; Score 9; DB 1; Length 434;
DR	ProDom; PD000779; Chorismate_bind; 1.	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	AC	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	ID	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	PRT;	453 AA.
DR	ProDom; PD000779; Chorismate_bind; 1.	Query Match	2.3%; Score 9; DB 1; Length 434;
DR	ProDom; PD000779; Chorismate_bind; 1.	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	AC	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	ID	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	PRT;	453 AA.
DR	ProDom; PD000779; Chorismate_bind; 1.	Query Match	2.3%; Score 9; DB 1; Length 434;
DR	ProDom; PD000779; Chorismate_bind; 1.	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	AC	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	ID	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	PRT;	453 AA.
DR	ProDom; PD000779; Chorismate_bind; 1.	Query Match	2.3%; Score 9; DB 1; Length 434;
DR	ProDom; PD000779; Chorismate_bind; 1.	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	AC	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	ID	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	PRT;	453 AA.
DR	ProDom; PD000779; Chorismate_bind; 1.	Query Match	2.3%; Score 9; DB 1; Length 434;
DR	ProDom; PD000779; Chorismate_bind; 1.	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	AC	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	ID	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	PRT;	453 AA.
DR	ProDom; PD000779; Chorismate_bind; 1.	Query Match	2.3%; Score 9; DB 1; Length 434;
DR	ProDom; PD000779; Chorismate_bind; 1.	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	AC	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	ID	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	PRT;	453 AA.
DR	ProDom; PD000779; Chorismate_bind; 1.	Query Match	2.3%; Score 9; DB 1; Length 434;
DR	ProDom; PD000779; Chorismate_bind; 1.	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	AC	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	ID	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	PRT;	453 AA.
DR	ProDom; PD000779; Chorismate_bind; 1.	Query Match	2.3%; Score 9; DB 1; Length 434;
DR	ProDom; PD000779; Chorismate_bind; 1.	Best local Similarity	100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	ProDom; PD000779; Chorismate_bind; 1.	AC	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	ID	Q9VIG5;
DR	ProDom; PD000779; Chorismate_bind; 1.	PRT;	453 AA.
DR	ProDom; PD000779; Chorismate_bind; 1.	Query Match	2.3%; Score 9; DB 1

RT	"Whole genome sequencing of meticillin-resistant <i>Staphylococcus aureus</i> ."	RP	SEQUENCE FROM N.A.
RT	STRAIN=CV_NIPPONBARE;	RC	STRAIN=CV_NIPPONBARE;
RL	Lancet 357:1225-1240(2001);	RA	Tozawa Y., Hasegawa H., Terakawa T., Wakasa K.;
DR	EMBL; AB03132; BAM42140.1; -.	RT	*Rice cDNA encoding anthranilate synthase alpha subunit."
KW	Complete proteome;	RL	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
SEQUENCE	453 AA; 52245 MW; EOFBD29C30B3161 CRC64;	DR	EMBL; AB022602; BAM82094.1; -.
SQ	[1]	DR	HSSP; Q00128; 1QDL;
Query Match	2.3%; Score 9; DB 2; Length 453;	DR	InterPro; IPR000350; Chorismate_bind;
Best Local Similarity	100.0%; Pred. No. 2.3;	DR	Pfam; PF00425; chorismate_bind; 1.
Matches	9; Conservative 0; Mismatches 0;	DR	PRINTS; PRO0005; ANTSNTHASET;
OY	298 LHPPPALGG 306	DR	ProDom; PD000779; Chorismate_bind; 1.
Db	355 LHPPPALGG 363	SQ	SEQUENCE 577 AA; 63947 MW; D880F8733809AC38 CRC64;
RESULT	10	Query Match	2.3%; Score 9; DB 10; Length 577;
ID	09KCB4 PRELIMINARY; PRT; 502 AA.	Best Local Similarity	100.0%; Pred. No. 2.9;
ID	09KCB4; PRT; 502 AA.	Matches	9; Conservative 0; Mismatches 0;
AC		OY	362 AGAGIVADS 370
DT	01-OCT-2000 (TREMBLrel. 15, Created)	Db	539 AGAGIVADS 547
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	RESULT	12
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	ID	09XU29 PRELIMINARY; PRT; 606 AA.
DE	ANTHRANILATE SYNTHASE.	AC	09XU29; PRT; 606 AA.
GN	TRPE OR BH1659.	DT	01-NOV-1999 (TREMBLrel. 12, Created)
OS	Bacillus halodurans.	DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;	DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
OX	Bacillus/Staphylococcus group; Bacillus.	DE	ANTHRANILATE SYNTHASE ALPHA 2 SUBUNIT.
NCBI_TAXID=86665;	[1]	GN	OSASA2.
RN		OS	Oryza sativa (Rice).
RP	SEQUENCE FROM N.A.	OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
RC	STRAIN=-125 / JCM 9153;	OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
RX	MEDLINE=20512582; Pubmed=11058132;	OC	Brachidae; Oryzeae; Oryza.
RA	Takami H., Nakasawa K., Maeno G., Sasaki R., Masui N.,	OX	NCBI_TaxID=4530;
RA	Fuji F., Hirama C., Nakamura Y., Ogashwara N., Kuwara S.,	RN	[1]
RA	Horikoshi K.;	RP	SEQUENCE FROM N.A.
RT	Complete genome sequence of the alkaliophilic bacterium <i>Bacillus halodurans</i> and genomic sequence comparison with <i>Bacillus subtilis</i> .";	RC	STRAIN=CV_NIPPONBARE;
RL	Nucleic Acids Res. 28:317-331(2000).	RA	Tozawa Y., Hasegawa H., Terakawa T., Wakasa K.;
DR	EMBL; AB001512; BAB05378.1; -.	RT	*Rice cDNA encoding anthranilate synthase alpha subunit.";
DR	InterPro; IPR000350; Chorismate_bind.	RL	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR	Pfam; PF00425; chorismate_bind; 1.	DR	EMBL; AB022602; BAM82095.1; -.
DR	PRINTS; PR0005; ANTSNTHASET;	DR	HSSP; Q06128; 1QDL;
DR	ProDom; PD000779; Chorismate_bind; 1.	DR	InterPro; IPR000350; Chorismate_bind.
KW	Complete proteome.	DR	ProDom; IPRO1680; W040.
SQ	SEQUENCE 502 AA; 56349 MN; D844E9AB2689551B CRC64;	DR	Pfam; PF00425; chorismate_bind; 1.
OY	352 AGAGIVADS 370	DR	PRINTS; PR0005; ANTSNTHASET;
Db	458 AGAGIVADS 466	DR	ProDom; PD000779; Chorismate_bind; 1.
RESULT	11	DR	PROSITE; PS00678; WD_REPEATS_1; UNKNOWN 1;
09KJ30	PRELIMINARY; PRT; 577 AA.	DR	SEQUENCE 606 AA; A74AB7CE986F0608 CRC64;
AC	09KJ30; PRELIMINARY; PRT; 577 AA.	OY	362 AGAGIVADS 370
AC	09KJ30; PRELIMINARY; PRT; 577 AA.	Db	567 AGAGIVADS 575
DT	01-NOV-1999 (TREMBLrel. 12, Created)	RESULT	13
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)	ID	09AJP3 PRELIMINARY; PRT; 55 AA.
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	AC	09AJP3; PRELIMINARY; PRT; 55 AA.
DE	ANTHRANILATE SYNTHASE ALPHA 1 SUBUNIT.	AC	09AJP3; PRELIMINARY; PRT; 55 AA.
DN	OSASAL.	AC	09AJP3; PRELIMINARY; PRT; 55 AA.
OS	Oryza sativa (Rice).	DT	01-JUN-2001 (TREMBLrel. 17, Created)
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
OC	Embryophyta; Oryzeae; Oryza.	DE	HYPOTHETICAL PROTEIN SPY0170.
OX	NCBI_TaxID=4530;	GN	SPY0170.
RN	[1]	OS	Streptococcus pyogenes.

OC Bacteria; Firmicutes; *Bacillus/Clostridium* group; Streptococcaceae;
 OC Streptococcus
 OC NCBI_TaxID=1314;
 RN [1]
 RP STRAIN=SF370;
 RC
 RX MEDLINE=21192684; PubMed=11296296;
 RA Ferretti J.J., Moshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
 PRIMEAUX C., Sezate S., Surovov A.N., Kenton S., Lai H.S., Lin S.P.,
 RA Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
 RT "Complete genome sequence of an M1 strain of *Streptococcus pyogenes*."
 RL PROC. Natl. Acad. Sci. U.S.A. 98:4653-4663(2001).
 EMBL; AE006486; AAC3270.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 55 AA; 5908 MW; B00EF0F07F137109 CRC64;

Query Match 2.0%; Score 8; DB 2; Length 55;
 Best Local Similarity 100.0%; Pred. No. 3; 5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 207 IATAAVAG 214
 |||||||
 DB 10 IATAAVAG 17

RESULT 14
 ID Q9I166 PRELIMINARY; PRT; 141 AA.
 AC Q9I166;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE HYPOTHETICAL PROTEIN PA2415.
 GN PA2415;
 OS *Pseudomonas aeruginosa*.
 OC Bacteria; Proteobacteria; gamma subdivision; pseudomonadaceae;
 OC pseudomonas.
 OC NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STRAIN=PAO1;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
 RA Hickey M.J., Brinkman F.S.L., Ruffnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Gooley L., Tolentino E., Westbroek-Wadman S., Yuan Y.,
 RA Brody B.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sauer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RA "Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an
 RR opportunistic pathogen."
 RL Nature 406:959-964 (2000).
 EMBL; AE004668; AAC05803.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 141 AA; 15171 MW; D6CC5F8B415421E0 CRC64;

Query Match 2.0%; Score 8; DB 2; Length 141;
 Best Local Similarity 100.0%; Pred. No. 8; 2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 ALGEALLA 234
 |||||||
 DB 125 ALGEALLA 132

RESULT 15
 Q9S169 PRELIMINARY; PRT; 387 AA.
 ID Q9S169
 AC Q9S169;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE F23N19.17.
 OC Arabidopsis thaliana (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N. A.
 RA Walker M., Shinn P., Brooks S., Buehler E., Chao Q., Dunn P., Khan S.,
 RA Kim C., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A.,
 RA Hansen N.F., Huizar L., Kremenevskaya I., Lenz C., Li J., Liu S.,
 RA Luoto S., Rowley D., Schwartz J., Toriumi M., Vysotskaya V., Yu G.,
 RA Davis R.W., Federer Spiel N.A., Theologis A., Ecker J.R.;
 RT "Genomic sequence for *Arabidopsis thaliana* BAC F23N19 from chromosome
 RT I.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -! COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC -! SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -! MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
 CC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).
 CC -! SIMILARITY: TO CLASS_I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOTRANSFERASES.
 DR EMBL; AAC07190; AA119543.1; -.
 DR HSSP; P00508; 7AA1.
 DR InterPro; IPR001511; Aminotran1.
 DR InterPro; IPR000796; Asp_Aminotransfse.
 DR Pfam; PF00155; aminotran_1.
 DR PRINTS; PR00799; TRANSAMINASE.
 DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
 KW Pyridoxal phosphate.
 SQ SEQUENCE 387 AA; 42723 MW; 5857C262340B9E1B CRC64;

Query Match 2.0%; Score 8; DB 10; Length 387;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 QOLXAALE 23
 |||||||
 DB 337 QOLXAALE 344

Search completed: March 27, 2002, 15:42:44
 Job time: 215 sec

Thu Mar 28 13:30:11 2002

us-08-774-104a-2.oli.rspt

GenCore version 4.5
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OM protein - protein search, using SW model

Run on: March 27, 2002, 15:34:44 ; Search time 24.81 Seconds
(without alignments)
1185.292 Million cell updates/sec

Title: US-08-774-104a-2

Perfect score: 397

Sequence: 1 MMTHETRALAQSDLQQLYA.....ETGSIKFEPMRQLLDYHVE 397

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 522463 seqs, 74073290 residues

Word size : 8

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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8: /SIDS8/gcgdata/geneseq/geneseq/PAI1987.DAT:*

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11: /SIDS8/gcgdata/geneseq/geneseq/PAI1990.DAT:*

12: /SIDS8/gcgdata/geneseq/geneseq/PAI1991.DAT:*

13: /SIDS8/gcgdata/geneseq/geneseq/PAI1992.DAT:*

14: /SIDS8/gcgdata/geneseq/geneseq/PAI1993.DAT:*

15: /SIDS8/gcgdata/geneseq/geneseq/PAI1994.DAT:*

16: /SIDS8/gcgdata/geneseq/geneseq/PAI1995.DAT:*

17: /SIDS8/gcgdata/geneseq/geneseq/PAI1996.DAT:*

18: /SIDS8/gcgdata/geneseq/geneseq/PAI1997.DAT:*

19: /SIDS8/gcgdata/geneseq/geneseq/PAI1998.DAT:*

20: /SIDS8/gcgdata/geneseq/geneseq/PAI1999.DAT:*

21: /SIDS8/gcgdata/geneseq/geneseq/PAI2000.DAT:*

22: /SIDS8/gcgdata/geneseq/geneseq/PAI2001.DAT:*

12 8 2.0 287 21 AAB08519 Protein encoded by
Human bone marrow
13 8 2.0 313 22 AAM00815 P. fluorescens ICS
14 8 2.0 331 20 AAV50335 E. coli ITC prote
15 8 2.0 391 20 AAV50335 P. fluorescens ICS
16 8 2.0 371 20 AAV50336 Human bone marrow
17 8 2.0 427 22 AAM00928 Human bone marrow
18 8 2.0 428 22 AAB05981 Human protein sequ
19 8 2.0 436 22 AAB4564 Tobacco anthranilia

Run on: March 27, 2002, 15:34:44 ; Search time 24.81 Seconds
(without alignments)
1185.292 Million cell updates/sec

ALIGNMENTS

RESULT 1
ID AAW69162 standard; Protein; 397 AA.

XX AC AAW69162;

XX DT 20-OCT-1998 (first entry)

XX DE Human neutral sphingomyelinase.

XX KW Human; neutral sphingomyelinase; N-Smase; diagnosis; Crohn's disease;

XX KW obesity; diabetes; Alzheimer's disease.

OS Homo sapiens.

XX PA 02-JUL-1998.

XX PD 23-DEC-1997; 97WO-US24051.

XX PR 24-DEC-1996; 96US-0774104.

XX WO9828445-A1.

XX (UWTO) UNIV JOHNS HOPKINS.

XX PI Chatterjee S;

XX DR WPI; 1998-37673/32.

DR N-FSDB; AAV41196.

XX PT Human neutral sphingomyelinase - used to, e.g. treat N-Smase

PT associated disorders, e.g. Crohn's disease, obesity, diabetes, and

PT Alzheimer's disease

XX PS Claim 19: Page 29-30; 47pp; English.

XX The present sequence represents human neutral sphingomyelinase (N-Smase).

CC A host cell containing a vector comprising a nucleotide sequence

CC encoding N-Smase can be used to produce N-Smase. N-Smase can be used in

CC a method for identifying a compound useful in the diagnosis or treatment

CC of a human neutral sphingomyelinase related disorder. N-Smase, and a

CC nucleotide sequence encoding N-Smase, can be used for modulating N-Smase

CC activity, and for treating a disorder associated with N-Smase. The

CC N-Smase disorders that can be treated with the nucleotide sequence or

CC N-Smase, is an inflammatory disorder, arthritis, osteoarthritis, Crohn's

CC disease, obesity, diabetes, cirrhosis, susceptible tumours, central

CC nervous system disorder, vascular restenosis, arterial occlusion arising

CC from plaque formation, cardiac disease where LV dysfunction occurs,

CC hypercholesterolaemia, cholesterol ester storage disorder, renal failure,

CC HIV infection, depression, schizophrenia, neurodegeneration, and

CC Alzheimer's disease. An antibody against N-Smase can be used to reduce

CC tumour necrosis factor alpha (TNF-alpha) induced apoptosis of mammalian

CC cells.

CC Maize C28 allele a

CC Maize anthranilate

CC E. coli entc prote

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	397	100.0	397 19 AAW69162	Human neutral sph
2	397	100.0	397 21 AAB08635	Amino acid sequenc
3	9	2.3	92 20 AAY42118	Wheat anthranilate
4	9	2.3	446 20 AAY42113	Corn anthranilate
5	9	2.3	577 20 AAW93815	Rice ASA first iso
6	9	2.3	577 20 AAW93816	Rice anthranilate
7	9	2.3	603 20 AAY42112	Corn anthranilate
8	9	2.3	606 20 AAW93814	Rice anthranilate
9	9	2.3	615 18 AAW76685	Maize C28 allele a
10	9	2.3	615 18 AAW76685	Maize anthranilate
11	8	2.0	271 20 AAV33698	E. coli entc prote

			Query Match	100.0%	Score 397; DB 19;	Length 397;	PS
			Best Local Similarity	100.0%	Pred. No. 0;	Mismatches 0;	XX
			Matches	397;	Conservative 0;	Mismatches 0;	XX
					Indels 0;	Gaps 0;	XX
							CC
QY	1	MMTYHETRALAQSDLQQLQYAALETTFCAYFAPADDPLRGIGAIATAKTAQALOGAVF	60				CC
Db	1	mmtyhettetralaqsdldlqqlyaalettefcaayfatpaddplrlfgialataktaqalggavf	60				CC
QY	61	GAQSFDCEYPQSELMAFGFWFVPEVMVIAADKITFGSDTWSFTWLAQFVKQPNTV	120				CC
Db	61	gaqsfdceyypqselmagfwfvpemvmtiaadkitfgsdtdfttwlaqfqpkqpntv	120				CC
QY	181	HVVLKRHDELFSTATPERLVAMMSGQATAAVAGTSRSGTDADDIALGEALLASOKNR	240				CC
Db	181	hvvkrhdelefstapervlvamsqgqataavagsrrtgddialgeallasknri	240				CC
QY	241	EHQYVVASITTRIQLQVTPGKPFMPLKQYHNPV	300				CC
Db	241	ehqyvvasittriqdvttskvpampsllknkqvhlytpitgdaahlsvtavidrlhp	300				CC
QY	301	TPALGGVPRREALYYIATHEKTRGLFAGPIGFTADNSGEFVGIRSMYVNQTORRATL	360				CC
Db	301	tpalggvpreaalyiathektrglfagpiyftadnsgefvgirsmyvnqgratil	360				CC
QY	361	FAGAGIVADSADQOYEETGLKEPMRLLQYHNPV	397				CC
Db	361	fagagivadsadqyeetgkifepmrqlkdynhve	397				CC
		RESULT 2					XX
AAB0835	ID	AAB0835 standard; Protein; 397 AA.					SQ
XX	AC		Query Match	100.0%	Score 397; DB 21;	Length 397;	PS
XX	AC	Best Local Similarity	100.0%	Pred. No. 0;	Mismatches 0;	Indels 0;	XX
XX	AC	Matches	397;	Conservative 0;	Mismatches 0;	Indels 0;	XX
XX	AC						XX
DT	20-DEC-2000	(first entry)					XX
XX	DE	Amino acid sequence of a human neutral sphingomyelinase (N-Smase).					XX
XX	DE	Human; neutral sphingomyelinase; N-Smase; anti-lipemic drug; SREBP-1; sterol regulatory element binding protein-1; serum cholesterol; LPL receptor; fatty acid synthesis; amyloid precursor protein; betaAPP; hyperlipoproteinemia; hypercholesterolemia; stroke; obesity; cirrhosis; cardiac disease; atherosclerosis; cerebral atherosclerosis; cholesterol ester storage disorder; organ transplantation failure; viral infection; encephalitis; liver disease.					XX
XX	OS	Homo sapiens.					OS
XX	PN	WO200050574-A1.					XX
XX	PD	31-AUG-2000.					XX
XX	PF	23-FEB-2-2000; 2000WO-US04657.					XX
XX	PR	24-FEB-1999; 990US-0121447.					XX
XX	PA	(UYJO) UNIV JOHNS HOPKINS.					XX
XX	PT	Chatterjee S;					XX
XX	DR	WPI; 2000-572085/53.					XX
XX	N-PSDB;	AAA64396.					XX
PT	Anti-lipemic drug comprising an effector of sterol regulatory element binding protein-1 for treating hyperlipoproteinemia, stroke, obesity, atherosclerosis, organ transplantation failure and cirrhosis						OS
PN	WO9949058-A2.						XX

XX
PD 30-SEP-1999.
XX
FT 19-MAR-1999; 99WO-US06046.
XX
PR 25-MAR-1998; 98US-0079386.
XX
(DUPO) DU PONT DE NEMOURS & CO E I.
PA
PI Vollmer SJ, Falco SC, Broglie RM, Bryan GT, Cahoon RE;
PT Rafalski JA;
XX
DR WPI; 1999-580451/49.
N-PSDB; AAZ25115.

XX
New isolated tryptophan biosynthetic enzyme nucleic acids, used to produce plants with altered tryptophan levels and for developing herbicides or fungicides -

XX
Claim 21; Page 64; 83pp; English.

XX
The present invention describes isolated anthranilate synthase alpha-subunit (ASAS), anthranilate synthase beta-subunit (ASBS), and tryptophan synthase alpha-subunit (TSAS) nucleic acids, and protein encoded by them, obtained from corn, rice, soybean and wheat cDNA libraries. The nucleic acid fragments may be used to create transgenic plants in which the disclosed ASAS, ASBS or TSAS are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found. This would have the effect of altering the level of tryptophan in those cells. Manipulation of the levels of some of the ASAS will also results in changes in the response to pathogen attack. Because this pathway is not followed for the production of tryptophan in higher animals, these enzymes are very good candidates for the discovery of herbicides and fungicides. The ASAS, ASBS or TSAS can be used as targets to facilitate design and/or identification of inhibitors of those enzymes that may be useful as herbicides. Nucleic acid fragments can also be used as probes for genetically and physically mapping the genes that they are a part of, and as markers for traits linked to those genes. Such information may be useful in plant breeding in order to develop lines with desired phenotypes. AAZ25109 to AAZ25127 represent specifically claimed nucleic acids from the present invention and AAY42112 to AAY42130 represent the proteins encoded by them.

XX
Sequence 92 AA;

Query Match 2.3%; Score 9; DB 20; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0;
Matches 9; Conservative 0; Indels 0; Gaps 0;

QY 362 AGAGIVADS 370
Db 53 agagivads 61

RESULT 4
AY42113
ID AAY42113 standard; Protein: 446 AA.
XX
AC AAY42113;
XX
DT 13-DEC-1999 (first entry)
DE Corn anthranilate synthase alpha subunit portion protein sequence.
XX
Anthranilate synthase alpha subunit; tryptophan biosynthetic enzyme; chimeric gene; corn; rice; soybean; wheat; tryptophan synthase; anthranilate synthase beta subunit; herbicide; fungicide; phenotype; pathogen attack; identification; transgenic plant; ASAS; ASBS; TSAS; plant breeding.
KW maize; wheat; tryptophan content; nutritional value.
OS Zea mays.

XX
FH Key
FT Misc-difference Location/Qualifiers
FT /note= "unspecified"
XX
PN WO949058-A2.
XX
PD 30-SEP-1999.
XX
PR 19-MAR-1999; 99WO-US06046.
XX
PR 26-MAR-1998; 98US-0079386.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Vollmer SJ, Falco SC, Broglie RM, Bryan GT, Cahoon RE;
PT Rafalski JA;
XX
DR WPI; 1999-580451/49.
N-PSDB; AAZ25110.

XX
New isolated tryptophan biosynthetic enzyme nucleic acids, used to produce plants with altered tryptophan levels and for developing herbicides or fungicides -

XX
Claim 21; Page 57-59; 83pp; English.

XX
The present invention describes isolated anthranilate synthase alpha-subunit (ASAS), anthranilate synthase beta-subunit (ASBS), and tryptophan synthase alpha-subunit (TSAS) nucleic acids, and protein encoded by them, obtained from corn, rice, soybean and wheat cDNA libraries. The nucleic acid fragments may be used to create transgenic plants in which the disclosed ASAS, ASBS or TSAS are present at higher or lower levels than normal or in cell types or developmental stages in which they are not normally found. This would have the effect of altering the level of tryptophan in those cells. Manipulation of the levels of some of the ASAS will also results in changes in the response to pathogen attack. Because this pathway is not followed for the production of tryptophan in higher animals, these enzymes are very good candidates for the discovery of herbicides and fungicides. The ASAS, ASBS or TSAS can be used as targets to facilitate design and/or identification of inhibitors of those enzymes that may be useful as herbicides. Nucleic acid fragments can also be used as probes for genetically and physically mapping the genes that they are a part of, and as markers for traits linked to those genes. Such information may be useful in plant breeding in order to develop lines with desired phenotypes. AAZ25109 to AAZ25127 represent specifically claimed nucleic acids from the present invention and AAY42112 to AAY42130 represent the proteins encoded by them.

XX
Sequence 446 AA;

Query Match 2.3%; Score 9; DB 20; Length 446;
Best Local Similarity 100.0%; Pred. No. 2; Mismatches 0;
Matches 9; Conservative 0; Indels 0; Gaps 0;

QY 362 AGAGIVADS 370
Db 408 agagivads 416

RESULT 5
AAW93815
ID AAW93815 standard; Protein: 577 AA.
XX
AC AAW93815;
XX
DT 25-JUN-1999 (first entry)
DE Rice ASA first isozyme alpha-subunit protein variant.
XX
KW Anthranilate synthase; alpha-subunit; ASA; rice; isozyme; plant; seed; maize; wheat; tryptophan content; nutritional value.
OS

OS	ORYZA SATIVA.
PT	synthase - used for improving tryptophan production and nutritional value of crops, e.g. rice, maize or wheat.
PN	WO9311800-A1.
XX	
PS	Claim 1; Page 128-131; 152pp; Japanese.
XX	
PD	11-MAR-1999.
XX	
PR	29-AUG-1998; 97JP-0235049.
XX	
PA	(HOKK) HOKKO CHEM IND CO LTD.
PA	(NOHQ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
XX	
PT	DNA encodes α -subunit of first isozyme of rice anthranilate synthase - used for improving tryptophan production and nutritional value of crops, e.g. rice, maize or wheat.
PT	WPI; 1993-228882/19.
DR	N-PDB; AAX23754.
XX	
PS	Claim 7; Page 145-147; 152pp; Japanese.
XX	
CC	This invention describes a novel rice anthranilate synthase first isozyme alpha-subunit. The encoding DNA can be used to produce transformant plants and seeds, of e.g. rice, maize or wheat, with enhanced tryptophan content and nutritional value of the crops.
CC	
CC	DNA encodes α -subunit of first isozyme of rice anthranilate synthase - used for improving tryptophan production and nutritional value of crops, e.g. rice, maize or wheat.
CC	
CC	This invention describes a novel rice anthranilate synthase first isozyme alpha-subunit. The encoding DNA can be used to produce transformant plants and seeds, of e.g. rice, maize or wheat, with enhanced tryptophan content and nutritional value of the crops.
CC	
SQ	Sequence 577 AA;
Db	539 agagivads 547
RESULT	7
ID	AY42112 standard; Protein; 603 AA.
XX	
ID	AY42112; AC AAY42112; DT 13-DBC-1999 (first entry)
XX	
DE	Corn anthranilate synthase alpha subunit protein sequence.
XX	
KW	Anthranilate synthase alpha subunit; tryptophan biosynthetic enzyme; chimeric gene; corn; rice; soybean; wheat; tryptophan synthase; anthranilate synthase beta subunit; herbicide; fungicide; phenotype; pathogen attack; identification; transgenic plant; ASAS; ASBS; TSAS;
KW	
KW	plant breeding; zea mays.
OS	
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 15 /note= "unspecified"
FT	Misc-difference 75 /note= "unspecified"
FT	Misc-difference 115 /note= "unspecified"
FT	
XX	
PN	W09311800-A1.
XX	
PD	30-SEP-1999.
XX	
PP	19-MAR-1999; 99WO-US05046.
XX	
PR	26-MAR-1998; 98US-0079386.
XX	
PA	(DUPO) DU PONT DE NEMOURS & CO E I.
XX	
PI	Vollmer SJ, Falco SC, Broglie RM, Bryan GT, Cahoon RE;
PI	Rafalski JA;
XX	
DR	WPI; 1993-580451/49.
DR	N-PDB; AAZ25109.
XX	
PT	New isolated tryptophan biosynthetic enzyme nucleic acids, used to produce plants with altered tryptophan levels and for developing herbicides or fungicides -
PT	
XX	
PS	Claim 21; Page 55-57; 83pp; English.
XX	
CC	The present invention describes isolated anthranilate synthase alpha-subunit (ASAS), anthranilate synthase beta-subunit (ASBS), and tryptophan synthase alpha-subunit (TSAS) nucleic acids, and protein
CC	

Query Match 2.3%; Score 9; DB 18; Length 615;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 362 AGAGIVADS 370
 Db 576 agagivads 584

|||||||

RESULT 10
 AAW26685 standard; Protein; 615 AA.
 XX
 AC AAY3698;
 XX
 DT 27-MAR-1998 (first entry)
 XX
 DE Maize anthranilate synthase alpha subunit.
 KW Anthranilate synthase; L-tryptophan; tolerance; resistance;
 KW transgenic plant; maize; selectable marker.
 OS zea mays inbred line Va26.
 XX
 FH Key Location/Qualifiers
 Peptide 1..46 /label= Transit_peptide
 FT
 XX
 WO9726366-A1.
 XX
 PD 24-JUL-1997.
 XX
 PF 17-JAN-1997; 97WO-US00983.
 PR 19-JAN-1996; 96US-0604789.
 XX
 PA (DEKA-) DEKALB GENETICS CORP.
 PI Anderson PC, Chomet PS, Griffon MC, Kriz AL;
 DR WPI; 1997-385350/35.

XX
 PT DNA encoding anthranilate synthase resistant to inhibition by
 PT tryptophan - and transformed plants, used e.g. to improve tryptophan
 PT levels in plants and as marker for cell selection
 XX
 PS Claim 7; Fig 3; 87pp; English.

XX
 CC This protein sequence comprises a maize anthranilate synthase (AS)
 CC alpha subunit encoded by a cDNA clone (see AAT0103) obtained from
 CC inbred line Va26. It differs at only 1 residue (Met-377 for Lys)
 CC from the alpha subunit (see AAW26685) of a maize allele C28 AS that
 CC is resistant to inhibition by free L-tryptophan or its amino acid
 CC analogues. Maize AS sequences, especially those from the C28
 CC allele, can be used in claimed methods: (i) to impart tolerance of
 CC plants to Trp analogues; (ii) to alter, particularly increase, the
 CC Trp content of plants, either to increase nutritional value or as a
 CC source of Trp by extraction; (iii) for production of recombinant AS
 CC (used for screening to identify agents that bind to or inhibit it);
 CC and (iv) for selection of transformed cells. Transgenic plants
 CC containing AS can be used for production of proteins or other
 CC compounds, including in vitro culture of their cells. The trait of
 CC resistance to Trp can be introduced to a wide variety of commercial
 CC maize lines.

SQ Sequence 615 AA;

Query Match 2.0%; Score 8; DB 20; Length 271;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 360 LFAGAGIV 367
 Db 238 lfqagiv 245

|||||||

RESULT 12
 AAB08519
 ID AAB08519 standard; Protein; 287 AA.
 XX
 AC AAB08519;
 XX
 DT 20-DEC-2000 (first entry)
 DE Protein encoded by haemoglobin-response gene HBR2.
 XX
 KW Haemoglobin-response gene; HBR1; HBR2; HBR3; haemoglobin; adhesion;
 disseminated infection; blastoconidia; fibronectin.
 XX
 OS Candida albicans.
 XX
 PN WO200050601-A2.
 XX
 PD 31-AUG-2000.
 XX
 PF 18-JAN-2000; 2000WO-US01184.
 XX
 PR 26-FEB-1999; 99US-0258634.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PT Roberts DD, Yan S;
 XX
 WPI; 2000-543913/49.
 XX
 PT detecting disseminated Candida albicans infections using
 hemoglobin-response genes and proteins, probes and antibodies derived
 from them -
 XX
 PS Claim 3; Page 50-51; 54pp; English.
 XX
 CC The present sequence is encoded by a haemoglobin-response
 gene HBR1 and HBR3. The expression of these genes is specifically
 induced when the organism is exposed to haemoglobin during disseminated
 infections. Haemoglobin induces increased adhesion of C. albicans
 blastoconidia to fibronectin. HBR1, HBR2 and HBR3 nucleic acid probes,
 proteins and antibodies are used for the diagnosis of disseminated
 C. albicans infections.
 XX
 SQ Sequence 287 AA;

Query Match 2.0%; Score 8; DB 21; Length 287;
 Best Local Similarity 100.0%; Pred. No. 13; Mismatches 8; Conservative 0; Indels 0; Gaps 0;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GAYFATPA 35
 Db 248 gayfatpa 255

RESULT 13
 AAM00815
 ID AAM00815 standard; Protein; 313 AA.
 XX
 AC AAM00815;
 XX
 DT 01-OCT-2001 (first entry)
 XX
 DE Human bone marrow protein, SEQ ID NO: 178.
 XX
 KW Human; bone marrow; antiinflammatory; cytostatic; neuroprotective;
 KW antiviral; antibacterial; antifungal; anti-HIV; haemostatic;
 KW immunosuppressive; gene therapy; cytokine cell proliferation;
 cell differentiation modulator; immune disorder; infection; cancer;
 human immunodeficiency virus; HIV; autoimmune disorder; haemophilia.
 XX

OS Homo sapiens.
 XX
 PN WO2001534960-A2.
 XX
 PD 26-JUL-2001.
 XX
 PR 23-DEC-2000; 2000WO-US34960.
 XX
 PR 21-JAN-2000; 2000US-04188725.
 PR 25-APR-2000; 2000US-0523317.
 PR 09-JUL-2000; 2000US-0528042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-066191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 30-NOV-2000; 2000US-0250583.
 XX
 PA (HYSEQ-) HYSEQ INC.
 XX
 PI Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Chen R, Ma Y;
 PI Ren F, Wang J, Werbman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Drmanac R;
 XX
 DR WPI; 2001-488707/5.
 DR N-PSDB; AHH8934.

OS Homo sapiens.
 XX
 PN Novel bone-marrow-expressed polynucleotides and polypeptides, useful
 for treating e.g. cancer and immune deficiency disorders.
 XX
 PS Claim 10; Page 334-335; 648pp; English.
 XX
 CC The present sequence is one of 251 novel human polypeptides encoded
 by a bone marrow-expressed polynucleotide. The polynucleotide and the
 polypeptide encoded by it are useful in the treatment of various
 immune deficiencies and disorders. The deficiencies and disorders may
 be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal
 infection, or may result from an autoimmune disorder, a coagulation
 disorder (e.g. haemophilia), inhibition of tumour cell proliferation,
 suppression of an inflammatory response or treatment of a nervous
 system disorder such as Alzheimer's disease. Detection of the presence
 or increased expression of the polynucleotide or the protein it
 encodes is useful for the diagnosis and/or prognosis of one
 or more types of cancer. The polynucleotide and polypeptide can be
 used as nutritional sources or supplements and in the screening of
 chemical compounds as potential drugs.
 XX
 SQ Sequence 313 AA;

Query Match 2.0%; Score 8; DB 22; Length 313;
 Best Local Similarity 100.0%; Pred. No. 14; Mismatches 8; Conservative 0; Indels 0; Gaps 0;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 151 VFGROOTL 158
 Db 157 vfgrqgtl 164

RESULT 14
 AAY0338
 ID AAY0338 standard; Protein; 331 AA.
 XX
 AC AAY0338;
 XX
 DT 14-JAN-2000 (first entry)
 XX
 DE P. fluorescens ICS orfA protein fragment.
 XX
 KW Isochorismate synthase; ICS; plant; pathogen resistance; chitinase;
 KW pathogen inducible promoter; antipathogenic protein; toxin;
 KW antifungal protein; albumin-type protein; hypersensitive response.
 XX
 OS Pseudomonas fluorescens.

XX WO9950423-A2.
 PN
 XX
 PD 07-OCT-1999.
 PF
 XX 25-MAR-1999; 99WO-EP02176.
 PR 31-MAR-1998; 98US-0080203.
 PR 03-APR-1998; 98US-0080625.
 PA (MOEB-) MOGEN INT NV.
 PA (UYLE-) RIJKSUNIV LEIDEN.
 PA (UYN-) UNIV NIJMEGEN.
 PA (MOEB-) MOGEN INT NV.
 PA (UYLE-) RIJKSUNIV LEIDEN.
 PA (UYN-) UNIV NIJMEGEN.
 XX Linthorst HJM, Verpoorte R, Verberne MC, Moreno PRH;
 PI Van Tegeelen LJP, Willems GJ, Croes AF, Stuiver MH, Custers J;
 PI Simons LH, Melchers LS, Bol JF;
 XX DR WPI; 1999-610056/52.
 DR N-PDB; AAZ23757.
 XX PT Method for inducing pathogen resistance in plants -
 PS Example 3; Page 58-59; 66pp; English.
 XX This invention describes a novel method for the induction of pathogen
 CC resistance in plants, by transformation with an expression cassette
 CC harboring a gene coding for an isochorismate synthase (ICS). A pathogen
 CC inducible promoter can be used to drive expression of a heterologous
 CC protein. The heterologous protein used in the method of the invention is
 CC an antipathogenic protein e.g. chitinase, glucanase, osmotin, lectins,
 CC saccharide oxidase, oxalate oxidase, magainins, toxins from *Bacillus*,
 CC *thuringiensis*, or antifungal protein isolated from *Mirabilis jalapa*,
 CC *Amaranthus*, *Raphanus*, *Brassica*, *Sinapis*, *Arabidopsis*, *Dahlia*, *Oncics*,
 CC *Lathyrus*, *Citteria*, *Allium* seeds, *Aralia* and *Impatiens* and albumin-type
 CC proteins, such as thionine, narin, barley trypsin inhibitor, cereal
 CC gliadin and wheat-alpha-amylase, or a protein that can induce a
 CC hypersensitive response, such as Cf, Bs3 and Po proteins from tomato and
 CC N-protein from tobacco. This sequence represents a *Pseudomonas*
 CC fluorescens isochorismate synthase orfA protein fragment which is
 CC described in the method of the invention.
 XX Sequence 331 AA;
 SQ Query Match 2.0%; Score 8; DB 20; Length 331;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 360 LFAGAGIV 367
 Db 297 lfagagiv 304
 RESULT 15
 AAY50335
 ID AAY50335 standard; Protein: 391 AA.
 XX AC AAY50335;
 XX DT 14-JAN-2000 (first entry)
 XX DE E. coli entC protein.
 XX KW Isochorismate synthase; ICS; plant; pathogen resistance; chitinase;
 KW pathogen inducible promoter; antipathogenic protein; toxin; entC;
 KW antifungal protein; albumin-type protein; hypersensitive response.
 XX OS Escherichia coli.
 XX PN WO9950423-A2.
 XX PD 07-OCT-1999.

XX 25-MAR-1999; 99WO-EP02176.
 XX
 PR 31-MAR-1998; 98US-0080203.
 PR 03-APR-1998; 98US-0080625.
 PA (MOEB-) MOGEN INT NV.
 PA (UYLE-) RIJKSUNIV LEIDEN.
 PA (UYN-) UNIV NIJMEGEN.
 XX Linthorst HJM, Verpoorte R, Verberne MC, Moreno PRH;
 PI Van Tegeelen LJP, Willems GJ, Croes AF, Stuiver MH, Custers J;
 PI Simons LH, Melchers LS, Bol JF;
 XX DR WPI; 1999-610056/52.
 DR N-PDB; AAZ23756.
 XX PT Method for inducing pathogen resistance in plants -
 XX PS Example 3; Page 51-53; 66pp; English.
 XX This invention describes a novel method for the induction of pathogen
 CC resistance in plants, by transformation with an expression cassette
 CC harboring a gene coding for an isochorismate synthase (ICS). A pathogen
 CC inducible promoter can be used to drive expression of a heterologous
 CC protein. The heterologous protein used in the method of the invention is
 CC an antipathogenic protein e.g. chitinase, glucanase, osmotin, lectins,
 CC saccharide oxidase, oxalate oxidase, magainins, toxins from *Bacillus*,
 CC *thuringiensis*, or antifungal protein isolated from *Mirabilis jalapa*,
 CC *Amaranthus*, *Raphanus*, *Brassica*, *Sinapis*, *Arabidopsis*, *Dahlia*, *Oncics*,
 CC *Lathyrus*, *Citteria*, *Allium* seeds, *Aralia* and *Impatiens* and albumin-type
 CC proteins, such as thionine, narin, barley trypsin inhibitor, cereal
 CC gliadin and wheat-alpha-amylase, or a protein that can induce a
 CC hypersensitive response, such as Cf, Bs3 and Po proteins from tomato and
 CC N-protein from tobacco. This sequence represents the *Escherichia coli*
 CC isochorismate synthase entC gene which is described in the method of
 the invention.
 XX Sequence 391 AA;
 SQ Query Match 2.0%; Score 8; DB 20; Length 391;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 360 LFAGAGIV 367
 Db 358 lfagagiv 365

Search completed: March 27, 2002, 15:39:37
 Job time: 293 sec

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OM protein - protein search, using sw mode1

Run on: March 27, 2002, 15:34:44 ; Search time 12.6 Seconds
(without alignments)
709.032 Million cell updates/sec

Title: US-08-774-104A-2
Perfect score: 397
Sequence: 1 MMVYHETRALAQSDLQQLYA.....ETGLKFEDPMRQLLKDYNHVE 397
Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 212252 seqs, 22503292 residues
Word size : 8
Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*

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- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	397	100.0	397	US-08-774-104A-2
2	9	2.3	604	Sequence 2, Appli
3	9	2.3	604	Sequence 2, Appli
4	9	2.3	604	Sequence 2, Appli
5	9	2.3	604	Sequence 2, Appli
6	9	2.3	621	Sequence 4, Appli
7	9	2.3	621	Sequence 4, Appli
8	8	2.0	616	Sequence 5, Appli

ALIGNMENTS

Query	Match	Length	Score	Best Local Similarity	Score	DB	Length	Score	Best Local Similarity	Score	DB	Length	Score
QY	1 MMVYHETRALAQSDLQQLYA.....ETGLKFEDPMRQLLKDYNHVE	60	100.0%	100.0%	397	DB	1 MMVYHETRALAQSDLQQLYA.....ETGLKFEDPMRQLLKDYNHVE	60	100.0%	397	DB	1 MMVYHETRALAQSDLQQLYA.....ETGLKFEDPMRQLLKDYNHVE	60
QY	61 GAQSFDCEQYPOSELMAGFWFPEVMVTAADKITEGSDTVSFTTWLAQFVKPQPNWT	120				Db	61 GAQSFDCEQYPOSELMAGFWFPEVMVTAADKITEGSDTVSFTTWLAQFVKPQPNWT	120			Db	61 GAQSFDCEQYPOSELMAGFWFPEVMVTAADKITEGSDTVSFTTWLAQFVKPQPNWT	120
QY	121 TSHVTDDEVWIERTENLDTIADQTTLAKVNGRQQTQLQLSDTIRLAQIRALAQNNTY	180				Db	121 TSHVTDDEVWIERTENLDTIADQTTLAKVNGRQQTQLQLSDTIRLAQIRALAQNNTY	180			Db	121 TSHVTDDEVWIERTENLDTIADQTTLAKVNGRQQTQLQLSDTIRLAQIRALAQNNTY	180
QY	181 HVVILKRHDLFLSATPERLUVAMMSGQIATAAVAGTSRGTDGADDIALGEALIASQRNRI	240				Db	181 HVVILKRHDLFLSATPERLUVAMMSGQIATAAVAGTSRGTDGADDIALGEALIASQRNRI	240			Db	181 HVVILKRHDLFLSATPERLUVAMMSGQIATAAVAGTSRGTDGADDIALGEALIASQRNRI	240
QY	241 EHQYVVAASITTRLQDVTSKLPVAMPMSLJKNKQVHQHLYTPITGDIAMHLSVIAIVDRHLHP	300				Db	241 EHQYVVAASITTRLQDVTSKLPVAMPMSLJKNKQVHQHLYTPITGDIAMHLSVIAIVDRHLHP	300			Db	241 EHQYVVAASITTRLQDVTSKLPVAMPMSLJKNKQVHQHLYTPITGDIAMHLSVIAIVDRHLHP	300
QY	301 TPALGVVREALLYIATHEKTRGLFARGPIGFADNSGEFWVGIRSSMVNQTORRATL	360				Db	301 TPALGVVREALLYIATHEKTRGLFARGPIGFADNSGEFWVGIRSSMVNQTORRATL	360			Db	301 TPALGVVREALLYIATHEKTRGLFARGPIGFADNSGEFWVGIRSSMVNQTORRATL	360
QY	361 FAGAGIVADSQOQEYETGKLFEPMRQLLKDYNHVE	397				Db	361 FAGAGIVADSQOQEYETGKLFEPMRQLLKDYNHVE	397			Db	361 FAGAGIVADSQOQEYETGKLFEPMRQLLKDYNHVE	397

RESULT 1 US-08-774-104A-2
; Sequence 2, Application US/08774104A
; Patent No. 5919687
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Subroto
; TITLE OF INVENTION: RECOMMENDANT N-SHASES AND NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dire, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA

RESULT 2 US-08-614-789B-2
; Sequence 2, Application US/086047898
; Patent No. 6118047

GENERAL INFORMATION:
 APPLICANT: Anderson, P.C.
 Chomet, P.S.
 Griffor, M.C.
 Kriz, A.L.

Kriz, A. L.

TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
 AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
 OVERPRODUCTION

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
 STREET: P.O. Box 2238
 CITY: Minneapolis
 STATE: MN
 COUNTRY: USA
 ZIP: 55402

COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 2.0

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

ATTORNEY/AGENT INFORMATION:
 NAME: Woessner, Warren D.
 REFERENCE/DOCKET NUMBER: 950.026US1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (612) 373-6903
 TELEFAX: (612) 339-3061
 TELEX: <Unknown>

PRIOR APPLICATION DATA:
 CURRENT APPLICATION DATA:
 FILING DATE: 19-Jan-1996
 APPLICATION NUMBER: US/08/604,789B

PRIOR APPLICATION DATA:
 CURRENT APPLICATION DATA:
 FILING DATE: 19-Jan-1996
 APPLICATION NUMBER: US/08/604,789B

PRIOR APPLICATION DATA:
 CURRENT APPLICATION DATA:
 FILING DATE: <Unknown>
 APPLICATION NUMBER: <Unknown>

ATTORNEY/AGENT INFORMATION:
 NAME: Woessner, Warren D.
 REFERENCE/DOCKET NUMBER: 950.026US1

REGISTRATION NUMBER: 30,440

REFERENCE/DOCKET NUMBER: 950.026US1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (612) 373-6903
 TELEFAX: (612) 339-3061
 TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:
 LENGTH: 604 amino acids
 TYPE: amino acid
 STRANDEDNESS: single

MOLECULE TYPE: protein
 TOPOLogy: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-08-604-789B-16

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-08-604-789B-2

Query Match 2.3%; Score 9; DB 3; Length 604;
 Best Local Similarity 100.0%; Pred. No. 0.88; Mismatches 0;
 Matches 9; Conservative 0; Indels 0; Gaps 0;

Qy 362 AGAGIVADS 370
 Db 565 AGAGIVADS 573

RESULT 4
 US-09-312-721A-2
 Sequence 2, Application US/09312721A
 Patent No. 6271016

GENERAL INFORMATION:
 APPLICANT: Anderson, P.C.
 Chomet, P.S.
 Griffor, M.C.
 Kriz, A.L.

TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
 AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
 OVERPRODUCTION

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
 STREET: P.O. Box 2938
 CITY: Minneapolis
 STATE: MN
 COUNTRY: USA
 ZIP: 55402

COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/312,721A
 PRIORITY NUMBER: 08/604,789
 FILING DATE: 17-May-1999
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/604,789
 FILING DATE: 19-JAN-1996

ATTORNEY/AGENT INFORMATION:

GENERAL INFORMATION:
 APPLICANT: Anderson, P.C.
 Chomet, P.S.
 Griffor, M.C.
 Kriz, A.L.

TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
 AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
 OVERPRODUCTION

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A.
 STREET: P.O. Box 2938
 CITY: Minneapolis
 STATE: MN

NAME: Woessner, Warren D.
 REGISTRATION NUMBER: 30,440
 REFERENCE/DOCKET NUMBER: 950,026US2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (612) 373-6903
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 604 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-312-721A-2

RESULT 5
 US-09-312-721A-16
 ; Sequence 16, Application US/09312721A
 ; Patent No. 6,271,016
 GENERAL INFORMATION:
 APPLICANT: Anderson, P.C.
 Chomet, P.S.
 Griffor, M.C.
 Kriz, A.L.
 TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
 AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
 OVERPRODUCTION
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Schweigman, Lundberg, Woessner & Kluth, P. A.
 STREET: P.O. Box 2938
 CITY: Minneapolis
 STATE: MN
 COUNTRY: USA
 ZIP: 55402
 COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/604,789B
 FILING DATE: 19-Jan-1996
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: <Unknown>
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Woessner, Warren D.
 REGISTRATION NUMBER: 30,440
 REFERENCE/DOCKET NUMBER: 950,026US1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (612) 373-6903
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 621 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-08-604-789B-4

Query Match 2,3%; Score 9; DB 3; Length 621;
 Best Local Similarity 100.0%; Pred. No. 0; 9;
 Matches 9; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

RESULT 6
 US-08-604-789B-4
 ; Sequence 4, Application US/08604789B
 ; Patent No. 6,118,047
 GENERAL INFORMATION:
 APPLICANT: Anderson, P.C.
 Chomet, P.S.
 Griffor, M.C.
 Kriz, A.L.
 TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
 AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
 OVERPRODUCTION
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Schweigman, Lundberg, Woessner & Kluth, P. A.
 STREET: P.O. Box 2938
 CITY: Minneapolis
 STATE: MN
 COUNTRY: USA
 ZIP: 55402
 COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/604,789B
 FILING DATE: 19-Jan-1996
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: <Unknown>
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Woessner, Warren D.
 REGISTRATION NUMBER: 30,440
 REFERENCE/DOCKET NUMBER: 950,026US1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (612) 373-6903
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 621 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-08-604-789B-4

Query Match 2,3%; Score 9; DB 3; Length 604;
 Best Local Similarity 100.0%; Pred. No. 0; 88;
 Matches 9; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

RESULT 7

US-09-3122-21A-4
Sequence 4, Application US/0931271A
Patent NO. 6210116
GENERAL INFORMATION:
APPLICANT: Anderson, P.C.
Chomet, P.S.
Griffor, M.C.
Kriz, A.L.

; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Macintosh Wordperfect converted to PC ASCII Text
; SEQ ID NO: 5
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-001-826-5

TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN OVERPRODUCTION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS: [REDACTED]

STREET: P. O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTY: USA
ZIP: 55402

COMPUTER READABLE FORM:
MATERIAL TYPE: Diskette

Search completed: March 27, 2002, 15:39:05
Job time: 261 sec

OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,721A
FILING DATE: 17-MAY-1999
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/604,789
FILING DATE: 19-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950.026USZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 373-6903
TELEFAX: (612) 339-3061
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 621 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-312,721A-4

```

Query Match          2.3%; Score 9; DB 4; Length 621;
Best Local Similarity 100.0%; Pred. No. 0; 9;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Qy   362 AGAGIVADS 370
      ||||| |
Db   570 AGAGIVADS 578

```

PATENT NO. 5,965,727
GENERAL INFORMATION:
APPLICANT: SONG, HEE-SOOK
APPLICANT: BROTHERTON, JEFFREY E.
APPLICANT: WIDHOLM, JACK M.
TITLE OF INVENTION: SELECTABLE MARKER AND PROMOTER FOR PLANT TISSUE CULTURE
TITLE OF INVENTION: TRANSFORMATION
FILE REFERENCE: UTO1.C1
CURRENT APPLICATION NUMBER: US/09/001,826A
CURRENT FILING DATE: 1997-12-31
EARLIER APPLICATION NUMBER: 08/937,739; 60/025,140
EARLIER FILING DATE: 1997-07-25; 1996-07-26

Thu May 28 13:30:10 2002

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